

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: February 27, 2003, 05:13:08 ; Search time 56 Seconds
(without alignments)
3543.212 Million cell updates/sec

Title: US-09-677-653A-50

Perfect score: 3374

Sequence: 1 MGDAQVAGSQRPHNRGRTRNV.....GRIARVARRARRARRAARAN 647

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 441362 segs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFMT=fastp -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humad40.cdi
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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6: /cgn2_6/ptodata/1/ina/Dackfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3374	100.0	2478	4	US-08-485-355B-47 Sequence 47, Appl
2	3374	100.0	2478	4	US-08-485-355B-49 Sequence 49, Appl
3	3374	100.0	2478	4	US-09-194-613-1 Sequence 1, Appl
4	3361	99.6	2479	4	US-08-485-355B-51 Sequence 51, Appl
5	294	8.7	6534	4	US-09-194-613-4 Sequence 4, Appl
6	139.5	4.1	3695	4	US-09-071-035-419 Sequence 419, App
7	139.5	4.1	3840	4	US-09-071-035-417 Sequence 417, App
8	125.5	3.7	2748	4	US-09-199-290-33 Sequence 33, Appl
9	124	3.7	4403765	4	US-09-103-840A-2 Sequence 2, Appl
10	121	3.6	3833	1	US-08-917-320-18 Sequence 18, Appl
11	121	3.6	3833	5	PCT-US95-04611A-18 Sequence 18, Appl
12	121	3.6	5931	3	US-08-783-774-1 Sequence 1, Appl

13	121	3.6	5931	4	US-09-556-706B-1 Sequence 1, Appl
14	121	3.6	4403765	4	US-09-103-840A-2 Sequence 2, Appl
15	121	3.6	4411529	4	US-09-103-840A-1 Sequence 1, Appl
16	120	3.6	2798	4	US-09-071-035-415 Sequence 415, App
17	120	3.6	3078	4	US-09-071-035-413 Sequence 413, App
18	117.5	3.5	4776	2	US-08-852-401-1 Sequence 1, Appl
19	117.5	3.5	1803	1	US-08-821-119-18 Sequence 18, Appl
20	117	3.5	1803	2	US-08-821-119-18 Sequence 18, Appl
21	117	3.5	3030	4	US-09-268-347-29 Sequence 29, Appl
22	117	3.5	30001	1	US-08-125-468-1 Sequence 1, Appl
23	117	3.5	30001	2	US-08-125-468-1 Sequence 1, Appl
24	116.5	3.5	1929	2	US-08-818-253-1 Sequence 1, Appl
25	116.5	3.5	1929	2	US-08-818-253-5 Sequence 5, Appl
26	116.5	3.5	1929	4	US-08-818-252-1 Sequence 1, Appl
27	116.5	3.5	1929	4	US-08-818-252-5 Sequence 5, Appl
28	116.5	3.5	1959	2	US-08-818-253-3 Sequence 3, Appl
29	116.5	3.5	1959	4	US-08-818-252-3 Sequence 3, Appl
30	116.5	3.5	1971	2	US-08-818-253-7 Sequence 7, Appl
31	116.5	3.5	1971	4	US-08-818-252-7 Sequence 7, Appl
32	116	3.4	2451	1	US-07-731-157A-3 Sequence 3, Appl
33	116	3.4	2451	1	US-08-229-448B-1 Sequence 1, Appl
34	116	3.4	2451	2	US-08-541-780-3 Sequence 3, Appl
35	115.5	3.4	3068	2	US-08-224-482-1 Sequence 1, Appl
36	115.5	3.4	3086	1	US-08-040-548-15 Sequence 15, Appl
37	115.5	3.4	3086	1	US-08-466-344-15 Sequence 15, Appl
38	115.5	3.4	3086	6	5206152-1 Patent No. 5206152
39	113.5	3.4	25165	4	US-09-453-702B-39 Sequence 39, Appl
40	113.5	3.3	2460	4	US-09-305-681-3 Sequence 3, Appl
41	113	3.3	2906	4	US-09-453-702B-186 Sequence 186, App
42	112.5	3.3	2923	1	US-08-243-542-6 Sequence 6, Appl
43	112.5	3.3	2923	1	US-08-477-407-6 Sequence 6, Appl
44	112.5	3.3	2923	1	US-08-484-355-6 Sequence 6, Appl
45	112	3.3	4411529	4	US-09-103-840A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-485-355B-47
Sequence 47, Application US/08485355B
Patent No. 6177075
GENERAL INFORMATION:
APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
TITLE OF INVENTION: Insect Viruses and Their Uses in Protecting Plants
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr Hobach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,355B
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS

	TELECOMMUNICATION INFORMATION:
?	TELEPHONE: (415) 781-1989
?	TELEFAX: (415) 398-3249
?	TELEX: 910 277299
?	INFORMATION FOR SEQ ID NO: 47:
?	SEQUENCE CHARACTERISTICS:
?	LENGTH: 2478 base pairs
?	TYPE: nucleic acid
?	STRANDEDNESS: unknown
?	TOPOLOGY: unknown
?	MOLECULE TYPE: DNA
?	FEATURE:
?	NAME/KEY: CDS
?	LOCATION: 283..753
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US-08-485-355B-47	
Alignment Scores:	
Pred. No.:	0
Score:	3374.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
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Db	426 CGGGTCAGCGGCACACCGTCACCGTCATAGTAGAAACCACACGCCGCTGGACCGGA 485
OY	41 ArgGlnValSerProPheAspAsnAsnPheThrAlaAlaAlaGlnAspLeuAlaGlnSerLeu 60
Db	486 AGCGAAGTTTCTCCCCCTGCAAAATTTCACCGCTGTGCACAGAAGCTCGCGAAGACCTT 545
OY	61 AspAlaAsnThrValThrPheProAlaAsnIleSerSerMetProGluPheArgAsnTrp 80
Db	546 GACGCCAACACCGTCACCTTCCCCTGCAATCATCTTAAGCATGCGCCGAATTCCGGAAATTGG 605
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Db	606 GCCAAGGAAAGATCGACCTCGACTCCGATTCATGGCTGACTCAAGTAACTTGAC 665
OY	101 ProAlaGlyAlaThrGlnSerAlaArgAlaValAlaGlyLysSerLysIleProAspGly 120
Db	666 CCACGGGGTCTACAGAGTCTGGCGCCGCCGTCGGGAGTACTCGAAGATCCCTACGCGC 725
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Db	786 GTCTCTACTGTCTCCCTCCCTCGACGGCGCCGCAATGAGGCTCTCGATTTTCTCTTT 845
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Db	846 CCGATGTTTCAGAACCCGCTACGTCCGCGTAGGAAGAGTGGAGAACAGAGATGTCGCTC 905
OY	181 AspValValAsnAspLeuIleGluTrpLeuAsnAsnLeuAlaAspTrpArgTryValVal 200
Db	906 GACCTTGTCAACGACCTCAACGCGATGGCTCAACAAATCTCCGACCTGGGCTTATCTCCTT 965
OY	201 AspSerGlnIleInrPrIleAsnPheThrAsnAspThrThyTryValArgIleArgVal 220
Db	966 GACTCTGAACAGTGGATTAACTTCAACCAATGACACACACTACTACGTCCGATCCGCGCTT 1023
OY	221 LeuArgProThrTryAspValProAspProThrGlnGlyLeuValArgThrValSerAsp 240

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Qy	241	TYrATgLeuThrTYrLYsAlAlAlerhCYsGlAlAlAsmEProThrLeuValAspGln	260
Dd	1086	TACCCGCTCACTTAAAGGGCATACATGTGAAGCCAACTGCACAACTCGTCACCA	1145
Qy	261	GLYpHeTPIIeGlyVgInTYrAlAlLeuThnProThSerLeuProGlnTYrAspAl	280
Dd	1146	GGCTTGTGGATCGGGCGAGCTAGGCTCTACCCCACTGACCTTACCGAGTACAGCGTC	1205
Qy	281	SerGluAlATrAlAlLeuHisThrLeuThrPheAlArGProSerSerAlAlAlAlLeu	300
Dd	1206	ACGAGGCGCTACGCTGACACACTTGTACCTTGCCAGACATCCAGCGCGCTGCACCTC	1265
Qy	301	AlAPheValITrPalAgLyLeuProGlnGlyTYhAlAProAlAgLYhThProAlArP	320
Dd	1266	GGTTTGTGTGGAGGTGGTCCACAGAGGGGACGCGCCCTGCAGAGCACTCCACCGGG	1325
Qy	321	GlUGlnAlAserSerGlyGlyTYrLeuThrTPrArGHisAsnGlyThrThrPheProAl	340
Dd	1326	GAGCAGGATCTCTGGGTGGCTACCTACCTGGCGGCACAGAGTACTCTTCCACACT	1385
Qy	341	GlySerValSerTYrValLeuProGlnGlyPheAlAlLeuGluArTYrAsProAsnAsp	360
Dd	1386	GGCTCCGTTACTCTACGTTTCCCTCGAGGGTTCGGCTTGCCTTACGCTACGACCCGAAC	1445
Qy	361	GlySerTPTrhArPheAlAserAlAgLYAsPThValThThPheArGlnValAlAlAl	380
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Qy	381	AspGluValValThThAsnAsnProAlAgLYGlySerAlAProThrPheThrVal	400
Dd	1506	GACGAGGTCTGTGTGACCAACAACCCCGCGGGGAGGAGCGCCCACTTCACCGCTG	1565
Qy	401	ArgValProProSerAsnAlATrThAsnThValPheArGAsnThLeuGlnThr	420
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Qy	421	ArgProSerSerArGArGLeuGluLeuProMetProProAlAspPheGlyGlnThrAl	440
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Qy	441	AlAlAsnAsnProLYsIlleGlnInSerLeuLeuLYsGlnThLeuGlyCYsTYrLeuVal	460
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Qy	461	HisSerLYsMeTArGAsnProValPheGlnLeuThnProAlASerSerPheGlyAlAlAl	480
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Qy	501	AspSerPheAspGlnAsnMetSerThrAlAlAlHisPheArGSerLeuSerHisSer	520
Dd	1866	GACTCATTTGCACAGACAATGTCACCGCTGTGGCCCACTTCGCTCACTCTCCACCTC	1925
Qy	521	CysSerIleValThrLYsThrTYrGlnGlyTPrGlnGlyValThAsnValAsnThPro	540
Dd	1926	TGCAGTATCGTCACTAGACCTACAGAGGTGGGAAGCGCTCACAGCACTCAACCGCT	1985
Qy	541	PheGlyGlnPheAlAlAlAlAgLYLeuLeuLYsAsnGlnGluTlleLeuCYsLeuAlAsp	560
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Qy	561	AspLeuAlArGLeuThrGlyValTYrProAlArAsAsnPheAlAlAlAlVal	580
Dd	2046	GACTGGCCACCCGCTCTACAGGTGTCTACCCCGCACTGACACTTGGCGCGCGCTT	2105
Qy	581	SerAlAlPheAlAlAlAsnMetLeuSerValLeuLYsSerGluAlArhSerSerIle	600
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 Db 1686 GCCAACACCCGAGATCGAGCTGCTCTTAAAGAAACACTTGCTGCTATTGTC 1745
 QY 461 HisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaVal 480
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 QY 481 SerPheAsnAsnProGlyTyrGluArgThrArgAspLeuProAspTyrThrGlyLeuArg 500
 Db 1806 TCCTTCAACATCGCGGTATAGCGGCACACCGGACTCCCGGACTACACTGGCATCCGT 1865
 QY 501 AspSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArgSerLeuSerHisSer 520
 Db 1866 GACTCATTCGACACGAACTGTCCACCGCTGTGGCCCACTTCGCTCATCTCCACTCC 1925
 QY 521 CysSerIleValThrThrThrTyrGlnGlyTyrGluGlyValThrAsnValAsnThrPro 540
 Db 1926 TCGAGTATGCTCACTAGACCTACAGGGTGGGAAGCGCTACGAACTCAACACGCGCT 1985
 QY 541 PheGlyGlnPheAlaHisAlaGlyLeuLeuLysAsnGluIleLeuCysLeuAlaAsp 560
 Db 1986 TTCGGCCAAATGCGCGACGCGGCGCTCCCAAGAAATGAGAGATCTCTCGCCGCGGAC 2045
 QY 561 AspLeuAlaThrArgLeuThrGlyValTyrProAlaThrAspAsnPheAlaAlaVal 580
 Db 2046 GACTCGGCGCACCGCTCTCAGAGTGTCTACCCGCGCACTGAACTTCCGCGCGCGCTT 2105
 QY 581 SerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGlnAlaThrSerSerIle 600
 Db 2106 TCTGCCCTTGGCGCAACATGCTCTCTCTGCTGAAAGTGGAGGCAACGTCCTTCATC 2165
 QY 601 IleLysSerValGlyGluThrAlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeuPro 620
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 QY 621 GlyLeuLeuMetSerValProGlyLysIleAlaAlaArgValAlaArgAlaArgAlaArg 640
 Db 2226 GGACTGCTAATAGTGTACAGGAAAGATTGCCGCGCGTCCGCGCGCGAGGCGCGC 2285
 QY 641 ArgArgAlaAlaAlaAlaAsn 647
 Db 2286 CGCGCGCGCTGTCGCAAT 2306

RESULT 3

; Sequence 1, Application US/09194613
 ; Patent No. 6251654
 ; GENERAL INFORMATION:
 ; APPLICANT: GORDON, Karl H.
 ; APPLICANT: HANZLIK, Terry N.
 ; TITLE OF INVENTION: MODIFIED SMALL RNA VIRUSES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDermott, Will & Emery

; STREET: 600 13th Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3096
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/194,613
 ; FILING DATE: 30-NOV-1998
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bucca Ph.D., Daniel
 ; REGISTRATION NUMBER: 42,368
 ; REFERENCE/DOCKET NUMBER: 50179-061
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-756-8000
 ; TELEFAX: 202-756-8087
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2478 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-194-613-1

Alignment Scores:
 Pred. No.: 0 Length: 2478
 Score: 3374.00 Matches: 647
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-677-653A-50 (1-647) x US-09-194-613-1 (1-2478)

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 QY 21 ArgValSerAlaAsnThrValThrValAsnGlyArgArgAsnGlyArgArgThrGly 40
 Db 426 CCGGTACGCGCCCAACACCGCTCACCGTCAATGTAGAACAAACACCGCGCTGGACCGGA 485
 QY 41 ArgGlnValSerProProAspAsnPheThrAlaAlaAlaGlnAspLeuAlaGlnSerLeu 60
 Db 486 AGGCAAGTTTCCCCCTGACAAATTTACCGCTGGTGGCAAGACCTGCGCAAGCGCTT 545
 QY 61 AspAlaAsnThrValThrPheProAlaAsnIleSerSerMetProGluPheArgAsnTrp 80
 Db 546 GAGCGCAACACCGTCACTTCCCGCTAACATCTAGCATCCCGGAATTCCGGAATTGG 605
 QY 81 AlaLysGlyLysIleAspLeuAspSerSerIleGlyTrpTyrPheLysTyrLeuAsp 100
 Db 606 GCCAAGGGAAGATGACTCGACTCCGATTCATCGGCTGCTCAAGTCAAGTCTTGAC 665
 QY 101 ProAlaGlyAlaThrGluSerAlaAlaArgAlaValGlyGluTyrSerLysIleProAspGly 120
 Db 666 CCAGCGGGTGTACAGAGTCTCGCGCGCGCGCTCGGCGGACTCGAAGATCCCTACGCGC 725
 QY 121 LeuValLysPheSerValAspAlaGluIleArgGluIleTyrAsnGluGluCysProVal 140
 Db 726 CTCGTCAAGTCTCCGTGACGACGAGATTAAGAGATCTATAAGAGAGAGTCCCGCCGTC 785
 QY 141 ValThrAspValSerValProLeuAspGlyArgGlnTyrPheSerLeuSerIlePheSerPhe 160
 Db 786 GTCACTGAGTGTCCGCTCCCTCGACGCGCGCGCTGAGAGCTCTCGATTCTTCCCTTT 845
 QY 161 PrometPheArgThrAlaTyrValAlaValAlaAsnValGluAsnLysGluMetSerLeu 180

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Db 846 CCGATGTCAGAACCGCTACGTCGCCGTAGGGAACGTGAGACAGAGATGTGCGTC 905
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Qy 181 AspValValAsnAspLeuIleGluTyrLeuAsnAsnLeuAlaAspTrrArgTyrValVal 200
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Db 906 GACGTGTCAAGACCTCCTACGATCGATGCGTCAACAAATCTCGCGACGTGGGTATGTGCTT 965
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Qy 201 AASPserGluGlnTrrPheAsnPherThrAsnAspThrThrTyrTyrValArgIleArgVal 220
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Db 966 GACTCTGAACAGATGATTAAGTCTACCAATGACACACGCTACTACGTCCGCAATCCCGCTT 1025
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Qy 221 LeuArgProThrTyrAspValProAspProThrGluGluValArgThrValSerAsp 240
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Qy 281 SerGluAlaTyrAlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAlaAlaLeu 300
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Db 1206 AGCGAGCGCTACGCTTGACACTTGGACCTTCGCCAGACATCCAGCGCGCTGCACATC 1265
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Qy 301 AlaPheValTrrPheAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrr 320
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Db 1266 GGGTTTGTGTGGGACAGTTGGCCACAGGGTGGACATGCGCTGCAGGACATCCAGCGCTG 1325
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Db 1446 GGCTCTTGGACCGACTTCTCCGCGAGGACACCGCTCACTTCCGGAGGCGCGCGTC 1505
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Qy 381 AspGluValValValThrAsnAsnProAlaGlyGlySerAlaProThrPheThrVal 400
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Qy 401 ArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuGluThr 420
|||
Db 1566 AAGATGCCCCCTCAAAACGCTTACACCAACACCGCTTTAGGAACAACGCTTAGAGACT 1625
|||
Qy 421 ArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnThrVal 440
|||
Db 1626 CGACCTCTCTCGTAGGGTCCGAACCTCCATGCGCACCTGTGACAGAGCGTTC 1685
|||
Qy 441 AlaAsnAsnProLysIleGluGlnSerLeuLeuLysGluThrLeuGlyCysTrrLeuVal 460
|||
Db 1686 GCCAACACCCGAAAGATCGACAGTGGCTTTAAAGAAACACTTGGCTGCTATTTGGTTC 1745
|||
Qy 461 HisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaVal 480
|||
Db 1746 CACTCCAAATGCGAAGACCCCGTTTCCAGCTCAGCCAGCGACGCTCCTTTGGCGCGT 1805
|||
Qy 481 SerPheAsnAsnProGlyTyrGluArgThrArgAspLeuProAspTrrArgIleArg 500
|||
Db 1806 TCCCTTAACAAATCCGGGTATGAGCGCACACCGGACCTCCCGGATACACTGCGCATCCCT 1865
|||
Qy 501 AspSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArgSerLeuSerHisSer 520
|||
Db 1866 GACTCTATTCAGACCAAGATGTCACCGCTGTGGCCACTTCGCTCCTCCACTCC 1925
|||
Qy 521 CysSerIleValThrLysThrTyrGlnGlyTrrPheGluGlyValThrAsnValAsnThrPro 540
|||

```

```

Db 1926 TGCATATCGTCACTAAGACTACAGGTTGGGAAGCGCGTCAAGAACTCAACAGCGCT 1985
|||
Qy 541 PheGlyGlnPheAlaHisAlaGlyLeuLeuLysAsnGluGluLeuCysLeuAlaAsp 560
|||
Db 1986 TTCGGCCAAATGCGCAGCCCGGCGCTCTCAAGAAATGAGAGATCTCTGCGCTCGCGAC 2045
|||
Qy 561 AspLeuAlaThrArgLeuThrGlyValTyrProAlaThrAspAsnPhaAlaAlaVal 580
|||
Db 2046 GACTGTGGCAACCGTCTCAAGGTGTCTACCCCGCCACATGACAACTTCGGGCGCGCTT 2105
|||
Qy 581 SerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThrSerSerIle 600
|||
Db 2106 TCGCGCTTGGCGCGCAATGCTGCTCCTCGCTGCTGAATCGGAGCAACGTCCTCATC 2165
|||
Qy 601 IleLysSerValGlyGluThrAlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeuPro 620
|||
Db 2166 ATCAAGTCCGTGGCGAGACTGCGCGCGCGGCTCACTCCGCGCTCCGGAAGCTACCC 2225
|||
Qy 621 GlyLeuLeuMetSerValProGlyLysIleAlaAlaArgValArgAlaArgAlaArg 640
|||
Db 2226 GGACTGCTAATGATGTACCAAGGAAATGTCGCGGTGTCCGCGCGCGAGCGCC 2285
|||
Qy 641 ArgArgAlaAlaArgAlaAsn 647
|||
Db 2286 CGCGCGCGCGCTGTCGAAT 2306
|||
RESULT 4
US-08-485-355B-51
; Sequence 51, Application US/08485355B
; Patent No. 6177075
GENERAL INFORMATION:
APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
TITLE OF INVENTION: Insect Viruses and Their Uses in
Protecting Plants
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,355B
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 2479 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA

```

FEATURE:
NAME/KEY: CDS
LOCATION: 283..2307
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-08-485-35B-51

Alignment Scores:

Pred. No.:	0	Length:	2479
Score:	3361.00	Matches:	647
Percent Similarity:	99.85%	Conservative:	0
Best Local Similarity:	99.85%	Mismatches:	0
Query Match:	99.61%	Indels:	1
DB:	4	Gaps:	0

US-09-677-653A-50 (1-647) x US-08-485-355B-51 (1-2479)

QY 1 MetGLyAPhAlAGLyVAlAlAsErGLnArPrOHlAsnArArGLyThrArGsNvAl 20
DB 366 ATGGGAGATGCTGGAGTGGCGCTCAGAGGACCTCAACCGTCGGGAACCGCTTAACGTT 425
Y 21 ArgValSerAlaAsnThrValThrValAsnGLyArGsAsnGLArGArGThrGLy 40
DB 426 CGGGTCACAGCCCAACACCGCTCACCTCAATGTTAGAAACCAACGCGCTGGACCGGA 485
QY 41 ArgGLnValSerProProAspAsnPhetThrAlaAlaGLnAspLeuAlaGLnSerLeu 60
DB 486 AGGCAAGTTTCTCCCTGACAAATTTCACCGCTGCTGCACAAAGACCTCGCGCAAGCCTT 545
QY 61 AspAlaAsnThrValThrPhe-ProAlaAsnLleSerSerMetProGLuPharAsnTr 80
DB 546 GACGGCAACACCGCTACTTTCCTCCCGCTAACATCTAGCAATGCCGAATTCCGGAAATTG 605
QY 80 PALAlaYsGLyLysLleAspLeuAspSerAspSerLleGLyTrpYrPheLysTrLeuAs 100
DB 606 GGCCCAAGGAAGATCGACCTCGACTCCGATTCCATCGGCTGTACTTCAAGTACCTTGA 665
QY 100 ProAlaGLyAlaThrGLnSerAlaArGLaValAlGLyLurYSerLysLleProAspL 120
DB 666 CCCACGGGTGCTACAGATGTGCGCGCGCTCGCGAGTACTCGAAGATCCTTGACGG 725
QY 120 YLeuValLysPheSerValAspAlaGLuLleArGLuLleTrpAsnGLuGLuCyProVa 140
DB 726 CCTCCTCAAGTCTCCGTCGACGAGATTAAGAGATCTATAACGAGGAGATGCCCGT 785
QY 140 lValThrAspValSerValProLeuAspGLyArGLnTrpSerLleSerLlePheSerPh 160
DB 786 CGTCACCTACGTCCTCCCTCCCTCGACGGCCGCAAGTGGACCTCTCGATTTTCTCCTT 845
QY 160 eProMetPheArGThrAlaTrValAlaValAlaAsnValGLuAsnLysGLuMetSerLe 180
DB 846 TCCGATGTTCAAGAACCGCGCTACGTCGCGGTAGCGAACGTCGAGAACAGAGATCTCGCT 905
QY 180 uAspAlValAlaAsnAspLeuLleGLuTrpLeuAsnAsnLeuAlaAspTrpArGLyValVa 200
DB 906 CGACCTTGTCAACGACCTCATCGAGTGGCTCAACAATCTCGCGCACTGCGGTATGTCGT 965
QY 200 lAspSerGLuGLnTrpLleAsnPhetThrAsnAspThrThrYrYrValAlaTrGLlArGVA 220
DB 966 TGACCTTAACAGTGGATTAATCTTACCAATGACACCAAGTACTACGTCCTCGATCCGGCT 1025
QY 220 lLeuArGProThrYrAspValProAspProThrGLuGLuLysValAlaTrGThrValSerAs 240
DB 1026 TCTACGCTCAACACTACGAGCTTCCAGACCCACAGAGGGCGCTGTGTCCAGACGTCACGA 1085
QY 240 pTyArGleuThrYrLysAlaAlaIleThrCyAGLlAlaAsnMetProThrLeuValAspGL 260
DB 1086 CTACCGCTCACTATTAAGGGGATTAACATGTGAACCAACAATGCGCAACACTCGTCGACCA 1145
QY 260 nGLYpHeTrpLleGLyGLnTrpAlaLeuThrProThrSerLeuProGLnTrpYrAspVA 280
DB 1146 AGGCTTTTGGATCGGGCGCGCTACGCTCTCAACCCCGACTAGCCTTACGGCAAGTACGAGCT 1205
QY 280 lSerGLuAlaTrValAlaLeuHlStrLeuThrPheAlaArGProSerSerAlaAlaAla 300

DB 1206 CAGCAGAGGCTACGCTCGACACTTGTACCTTCCCGACACATCCACGCGCGTGCACAT 1265
QY 300 uAlaPheValTrpAlaGLyLeuProGLnGLyGLnThrAlaProAlaGLyThrProAlaTr 320
DB 1266 CGCGTTTGTGTGGAGGTTTGGCCACAGGGTGGCACTGGCTGGACGACCTCCAGCGCTG 1325
QY 320 pGLuGLnAlaSerSerGLyGLyTrLeuThrTrpArGHisAsnGLyThrThrPheProAl 340
DB 1326 GGAGCAGGATCTCTGGGGGTCTACTCACTCGGGGCCAACAGGTACTACTTCCAGC 1385
QY 340 aGLySerValSerYrValLeuProGLuGLyPheAlaLeuGLuArGLyTrpAspProAsnAs 360
DB 1386 TGGCTCCGTTACCTACGTTCTCCCTGAGGGTTTCCCGCTTGAGCCCTAGACCCCAAGCA 1445
QY 360 pGLySerTrpThrAspPheAlaSerAlaGLyAspThrValThrPheArGGLnValAlaVa 380
DB 1446 CGGCTTGTGGACCGACTTTCGTCGCGAGGACACCGTCACTTTCGCGAGTGCCTG 1505
QY 380 lAspGLuValAlaValThrAsnAsnProAlaGLyGLyGLySerAlaProThrPheThrVa 400
DB 1506 CGACGAGGTCGTTGTGACCAACAAACCCCGCGCGCGGCGGACGCGCCCACTTACCGCT 1565
QY 400 lArGLyAlProProSerAsnAlaTrThrAsnThrValPheArGsAnThrLeuGLuTh 420
DB 1566 GAGATGCGCCCTTCAAAAGCTTACACCAACACCGTGTTAGGAACAGCTCTTAGAGAC 1625
QY 420 rArGProSerSerArGLyGLuLeuProMetProProAlaAspPheGLnThrVa 440
DB 1626 TCGACCTCTCTCTGTAGGCTCGAACTCCCTTAGGCACTGTGTGGACAAACGCTT 1685
QY 440 lAlaAsnAsnProLysLleGLuGLnSerLeuLeuLysGLuThrLeuGLyCySTYrLeuVa 460
DB 1686 CGCCAAACACCGAAGATCGACACTCGCTTTAAAGAAACACTTGGCTGTATTTCGT 1745
QY 460 lHisSerLysMetArGsAnProValPheGLnLeuThrProAlaSerSerPheGLyAlaVa 480
DB 1746 CCACCTCAAAATGCGAAACCCCGTTTCCAGCTCACCGCACGACACTCTTGTGGCGCGCT 1805
QY 480 lSerPheAsnAsnProGLyTrpGLuArGLnThrArGsPleuProAspYrThrGLyLleAr 500
DB 1806 TTCTTTCACAACATTCGGGTATAGACGCGACACGCACTCCCGGACTACACTGGCATCGG 1865
QY 500 gAspSerPheAspGLnAsnMetSerThrAlaValAlaHisPheArGSerLysSerHisSe 520
DB 1866 TGACATCATTCGACCAAGACATGTCCACCGCTGTGGCCCACTTCCGCTACATCTCCACTTC 1925
QY 520 rCySerLleValThrLysThrYrGLnGLyTrpGLuGLyValThrAsnValAsnThrPr 540
DB 1926 CTGCAGTATCGTCACTAAGACTTACCAAGGTTGGGAAGCGCTCAAGACGTCAACACGCGC 1985
QY 540 oPheGLyGLnPheAlaHisAlaGLyLeuLeuLysAsnGLuLleLeuCyStLeuAlaAs 560
DB 1986 TTTTCGGCAATTCGGCGACCGGGGCTCTCTCAAGATATAGAGATCTCTCCCTCGCGGA 2045
QY 560 pAspLeuAlaThrArGLyLeuThrGLyValYrYrProAlaThrAspAsnPheAlaAlaAlaVa 580
DB 2046 CGACCTGGCCACCGCTGTACAGAGTGTCTACCCCGCACTACAAACTCGGGGCGCGCT 2105
QY 580 lSerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGLuAlaThrSerSerIl 600
DB 2106 TTTCTCCCTTCCCGCGCAACATGCTCTCTCCGCTGTGAAGTCGGAGCGAACGTCCTCAT 2165
QY 600 eLleLysSerValGLyGLuThrAlaAlaGLyAlaAlaGLnSerGLyLeuAlaLysLeuPr 620
DB 2166 CATCAAGTCTCGTGGCGGAGCTGCGTGGCGGGCTCAAGTCCGGCTCGGGAAGCTACAC 2225
QY 620 nGLYLeuLeuMetSerValProGLyLysLleAlaAlaArGLyAlaArGLaArGLaAr 640
DB 2226 CGGACTGTATATGACTGTACCAAGGAAGATTGCCGCGGTCTCCGCGGCGCGCGAGCGCG 2285
QY 640 gArGArGLaAlaArGLaAsn 647

Db 2286 CCGCGCCGCGCTGTCGAAT 2307

RESULT 5

US-09-194-613-4

Sequence 4, Application US/09194613

Patent No. 6251654

GENERAL INFORMATION:

APPLICANT: GORDON, Karl H.

APPLICANT: HANZLIK, Terry N.

TITLE OF INVENTION: MODIFIED SMALL RNA VIRUSES

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDermott, Will & Emery

STREET: 600 13th Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3096

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/194,613

FILING DATE: 30-NOV-1998

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Bucca Ph.D., Daniel

REGISTRATION NUMBER: 42,368

REFERENCE/DOCKET NUMBER: 50179-061

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-756-8000

TELEFAX: 202-756-8087

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 6534 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-194-613-4

Alignment Scores:

Pred. No.:	3 226-20	Length:	6534
Score:	294.00	Matches:	184
Percent Similarity:	37.50%	Conservative:	74
Best Local Similarity:	26.74%	Mismatches:	281
Query Match:	8.71%	Indels:	151
		Gaps:	35

US-09-677-653a-50 (1-647) x US-09-194-613-4 (1-6534)

QY 2 G1YAspAlaGlyValAlaSerGlnArgProHisAsnArgGlyThrArgAsnValArg 21

Db 4012 GGGCAACGAGGGCGCGCAACAAACAACAGCTGACGACGAGGCGGGCTTAA 4071

QY 22 ValSerAlaAsnThrValThrValAsnGlyArgArgAsnGlnArgArgGlyArg 41

Db 4072 CTTCGCCCGTAGTCGACGAGATP----- 4095

QY 42 GlnValSerProProAspAsnPhetThrAlaAlaAlaGlnAspLeuAlaGlnSerLeuAsp 61

Db 4096 ---ACGAGCCCGCAGATGGCCGGAACCCGAAAC-----CAC 4128

QY 62 AlaAsnThrValThrPheProAlaAsnIleSerSerMetProGluPheArgAsnTrpAla 81

Db 4129 GCGAACAACCGGCTCAAC-CCGCGCTG-----GACACGCGTGAAGGGGCT 4172

QY 82 LysGlyLysIleAspLeuAsp-----SerAspSerIleGlyTyrTyrPheLysTyr 98

Db 4173 AAGGCAAGCATGATGAGAGTCCCATGTCAGCAGCATCAAGCATGATGATTCACGACTAT 4232

QY 99 LeuAspProAlaGlyAlaThrGlnSerAlaArgAlaValGlyGluTyrSerLysIlePro 118

Db 4233 CTAGACCCGAGCAGGAGATACAAAGACGCTGGACAGACGG-----AAATTC 4283

QY 119 AspGlyLeuValLysPheSerValAspAlaGluIleArgGluIleTyrAsnGluGly 138

Db 4284 GACGGCGGATACCTGATCAACATGCGGTCAATTGTGAGGAGACCGGGCGCCAGTAC 4343

QY 139 ProValValThrAspValSerValProLeuAspGlyArgGlnTyrSerLeuSerIlePhe 158

Db 4344 CCGGAGCTGAATTCTACAGCTCCCTGATGGCGGAGCTGCTCTAGTATG 4403

QY 159 SerPheProMetPheArgThrAlaTyrValAlaValAlaAsnValGluAsnLysGluMet 178

Db 4404 CATCTCCGTTCTTCAGGCATCCGTGTGTTCATCCACCACCACCAACGAA- 4460

QY 179 SerLeuAspValValAsn---AspLeu-----IleGluTyrLeuAsnLeu 193

Db 4461 ---GTGAGAGTACGAACGCGCATCTGATGCTGCGGAACGATGG---AACACAGG 4514

QY 194 AlaAspTyrArgTyrValValAspSerGluGlnIleThrIleAsnPheThrThr 213

Db 4515 ACGGAGCTGACCGAAGCGAGC---TACCAAGTTGGCGGAGAGTGGGAA- 4565

QY 214 TyrTyrValArgIleArgValLeuArgProThr-----TyrAspValProAspPro 230

Db 4566 TTTTACATGGTCGTC-----CCGACGAGCCGTGACGAGGATACCCCG 4613

QY 231 ThrGlu---GlyLeuValArgThrValSerAspTyrArgLeuThrTyrLysAlaIleThr 249

Db 4614 ACTGATCGGTGTATGAGGTTACTGAGAGTACCGTGTGATGAGAGCGGCTACA 4673

QY 250 CysGluAlaAsnMetProThrLeuValAspGlnIlePheThrIleGlyGlnTyrAla 269

Db 4674 GCGTACTTCAACGACGACCTCTGTGATGAGGAGTGGCGGATCGGCACTTC- 4730

QY 270 LeuThrProThrSerLeuProGlnIleTyrAspValSerGluAlaTyrAlaLeuIleThrLeu 289

Db 4731 ---CAACCGGACAAAGAACACACAGAGAAACCCGACATAGTACCGGACCCAA 4787

QY 290 Thr-----PheAlaArgProSerSerAlaAlaAlaLeuAlaPhe 302

Db 4788 ACGGCGGAGACGTACAGCTCGCGGTTCAAGCGCAATCAATGATGACATGAC- 4844

QY 303 ValThrAlaGlyLeuProGlnIleGlyThrAla---ProAlaGlyThrProAlaThrGlu 321

Db 4845 ATCGGGAGCAGCGTCGATTCGGGGGCGCAGCAATCCCGTACCCAGGTGTGATGGG 4904

QY 322 GlnAlaSerSerGlyGlyTyrLeuThrTyrArgIleAsnGlyThrThrPheProAlaGly 341

Db 4905 CCGATCCCGAGCTCGGCGAGCTGTGTCAGACTCGAAGCTGACATTCGACGTGCGA 4964

QY 342 -----SerValSerTyrValLeuProGlnIlePheAlaLeuGluArgTyrAspPro 358

Db 4965 AACACATACACATCACAGACAGCTGCGACACAGGTCGG- 5006

QY 359 AsnAspGlySerTyrThrAspPheAlaSerAlaGly---AspThrValThrPheArgGln 377

Db 5007 ---ACGGGAATGTGCAATTCCAGCAGCAGCGGAGCGGACCGTGGACC- 5054

QY 378 ValAlaValAspGluValValValThrAsnAsnProAlaGlyGlySerAlaProThr 397

Db 5055 ---GTGAC-----GGGGAGG- 5069

QY 398 PheThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeu 417

Db 5070 ---ACTGACGCGTTCGAGAGGATTTGACGCGCTCGAAGTATGCGAGCATCA 5126

QY 418 LeuGluThrArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGly 437

Db 5127 CTCATCAAGATTCACCAAC-----GACATGAACCCAAATGATGAGGCG 5171

QY 438 GlnThrValAlaAsnAsnProLysIleGluGlnSerLeuLeuLys-GluThrLeuGlyC 457

DB 5172 -----AACGGCAAGACCATTCAGTTCACACTAACGAACGAGGCGATTATATG 5219
QY 457 sTYrLeuValHisSerLysMetArgAsnProValPheGluLeuThrProAlaSerSeph 477
DB 5220 CCGG-----AGCGCTCAATCCGCTGTTCGAATGCAAT-CCGACGCTTGA 5293
QY 477 eglYAlaValSerPheAsnAsnProGlyTYrGluArgThrArgAsp----LeuProAspT 496
DB 5264 TGGACCGGTGGAT-----GAAAGACACCGAGAGACAACTGTGTATATT 5305
QY 496 yThrGly-----TleArgAspSerPheAspGlnAsnMetSer----- 508
DB 5306 ACACCGGCAATTGTGCTACTCCAGAGATACATCGACACACTTGCATAGATTGCC 5365
QY 509 -----ThraAlaValAlaHis-PheArgSerLeuSerHisSerCysSerIleValThr 525
DB 5366 GTCGATGACCGGTATGCTATCAATCAACCGTACCTTCCAGAGTTCGACGCTTCG 5425
QY 526 LysThrTYrGln-GlyTYrPgluGlyValThrAsnValAsnThrProPheGlyGlnPheAl 545
DB 5426 AAGCATACCGGGGAGGAGGAG-----CCTTGGGGCCCTTCGC 5464
QY 545 aHsAlaGlyLeuLeuLysAsnGluIleLeuCysLeuAlaAspLeuAlaThrAr 565
DB 5465 TACTGGGACACTCCGAAAGACGACGTGGCGCTAACAGTGTGCTGAACCTTGACCGATCT 5524
QY 565 glauThrGlyValTYrProAlaThrAspAsnPheAlaAlaValSerAlaPheAlaAl 585
DB 5525 GCACCATTCGCAATCCCGGAACGATACACGATTCGGGGCCCTATTCGCGATGTGGC 5584
QY 585 aAsnMetLeuSerSerValLeuLysSerGluAlaThrSerSerIleLeuLysSerValG 605
DB 5585 CAAGACCATAGCCCAATACCTCGC-----TATGTGGATCA----- 5621
QY 605 ygluThrAlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeuProGlyLeuLeuMetSe 625
DB 5622 -----GCAGCCGAGGTGGCGAATCCGCTGAGCAGACTGCATGAGAGCCGACCGAG 5674
QY 625 rValProGlyLysIleAlaAlaArgValArgAlaArgArgAlaArgArg----- 641
DB 5675 TGTAGCTCGAATTCACACCTCCGAGAGGCGGACGACGAGCAGACGACGATGTGGCGAAT 5734
QY 642 ----ArgAlaAlaArg 645
DB 5735 CGCTCGAGAGGCCCGC 5750

RESULT 6
US-09-071-035-419
Sequence 419, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: GILL H. CHOI
TITLE OF INVENTION: Enterococcus faecalis polynucleotides and polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEO ID NO: 419:
SEQUENCE CHARACTERISTICS:
LENGTH: 3695 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-071-035-419

Alignment Scores:
Pred. No.: 0.000308 Length: 3695
Score: 139.50 Matches: 140
Percent Similarity: 31.38 Conservative: 95
Best Local Similarity: 18.698 Mismatches: 247
Query Match: 4.138 Indels: 267
DB: Gaps: 31

US-09-677-653A-50 (1-647) x US-09-071-035-419 (1-3695)

QY 19 AsnValArgValSerAlaAsnThrValThrValAsnGlyArgAsnGlnArgArg 38
DB 1625 AACCGCAAGTCAACCGAAGCTTCGTAGACACCAAGCGCGCTAA----- 1669
QY 39 ThrGlyArgLysSerProProAspAsnPheThrAlaAlaAlaGlnAspLeuAlaGln 58
DB 1670 -----ATCACACCGCCACAGAGGTTCACCCCAAGTAAAGGATGATTACA 1717
QY 59 SerLeuAspAlaAsnThrVal-----ThrPheProAlaAsnIleSerSer--- 73
DB 1718 AGC---GACGCCCTACACTTTCACAAAGCAGCAGCAGCCTTACCAACACTTACACACAGGC 1774
QY 74 -----MetProGluPheArgAsnTrpAlaLysGlyLysIleAspLeuAspSer 91
DB 1775 GTTAAGCCTCAAGTTCACAAAGTGTGTACAAAGGCAAGTCCATTCTCAACACATTGACA 1834
QY 92 IleGlyTrpTrpPheLysTYrLeuAspProAlaGlyAlaThrGluSerAlaArgAlaVal 111
DB 1835 ACT----- 1837
QY 112 GlyGluTYrSerLysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArg 131
DB 1838 -----ACCAAGCCGCAAGTTATCAAGTGACCTGACGATGACAAATGATGATTGGAAT 1888
QY 132 GluIleTYrAsnGluLysCysProValValThrAspValSerValProLeuAsp----- 149
DB 1889 GTGGTGTATGACAAAGAACAGTGTAGACAGTATCATCATCATCATATGAACCTTGTG 1948
QY 150 -----GlyArgGlnTrpSerLeu 155
DB 1949 AATGAAAAAGCGGCGCTTTCACACCGCGGTAACTTTAGTGTGAAGTACTATGCGCAA 2008
QY 156 SerIlePheSerPheProMetPheArgThrAlaTYrValAlaValAsnValGluAsn 175
DB 2009 AGTACGAGTGCCTAC-----TTAAGACCGATTATTAAGCTGACCTCAAAAAATAAT 2062
QY 176 -----LysGluMetSerLeuAspValAlaAsnAspLeu 186
DB 2063 GGTAAATGGCAATATACGGTAAGTATTAATATGTAGTATGCAATTCGCCAAGATTA 2122
QY 187 IleGluTrpLeuAsn----- 191
DB 2123 TTGAATAAATATATATATGAGACAAACCAATCAGTGTACCAACAGATTACAGTTAATGTT 2182
QY 191 ----- 191
DB 2183 GATTAATTAGCATGACCAACAACTAAATATGTTGACAGCATTCATTAATGACACAGCT 2242

QY 192 -----AsnleualaasprArgTyrValVal----- 200
 Db 2243 CAAGAGTGAATCTGAATCCCTATGATATGTGTACACGACAAATAGTCTACTGGTTTC 2302
 QY 201 -----AspSerGluGlnTrpIleAsn 207
 Db 2303 GACCCAAATGTAGACACGACAGAGTTGACCTTATGATTCAGAAATCTCTTAACCTGCTTAAT 2362
 QY 208 PheThrAspAspThrThrTyr----- 215
 Db 2363 TTTGATTCAGATGCGACCTATTCTTAATGCAAAATATAGACTTTTTCACACGCAATTA 2422
 QY 216 -----ValArgIleArgValIleuArgProThrTyrIleVal----- 227
 Db 2423 GGATATAGTGGCACACGACAGAGTTAACTCTCTGTAATGTTCTTTTAAAGCCAAA 2482
 QY 228 ProAspProThrGluIleuValArgThrValSerAspTyrArgLeuThrTyrIleVal 247
 Db 2483 CCGCGGATATAGTCAAAACTGTCT-----TACAAAGTCACTCGCAACAA 2527
 QY 248 IleThrCysGluAlaAsnMetProThrIleuValAspGlnIlePheTrpIleGlyGln 267
 Db 2528 GTCACC-----GAAAACCTTCGTGGAT-----GTCAACGGGTGCC 2560
 QY 268 TyrAlaIleuThrProThrSerIleuProGlnTyrAspValSerGluAlaTyrAlaIleuHis 287
 Db 2561 AAAATCAGTCGACCAACAGGCTTCACCCAA-----GATACCAAGTACCAATGAAAC 2611
 QY 288 ThrLeuThrPheAlaIleuArgProSerSerAlaIleuAlaIleu----- 300
 Db 2612 AGTAAACACCTTC-----AAGTACACAGCGGCAAAAGCTTTACACGAGCATTAACAGT 2668
 QY 301 -----AlaPheValTrpAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyTrpPro 318
 Db 2669 GGCAAAGTCTATACGTTCCAAAGGGGTGTATAAAGGAAACCAAGCAATAGCTTG--- 2725
 QY 319 AlaTrpGluGlnAlaSerSerGlyGlyTyrLeuThrTrpArgHisnGlyTrpPhe 338
 Db 2726 -----AACAAACACCAACT 2740
 QY 339 ProAlaGlySerValSerTyrValLeuProGluGlyPheAlaLeuGluArgTyrAspPro 358
 Db 2741 CCAAAGCTCAATCGAC-----TTTGATGGC 2767
 QY 359 AsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnVal 378
 Db 2768 AATGACGATATGACCGCATGTATAGGAAGAAATACCAACAGCTAGTGCACATTAACT 2827
 QY 379 AlaValAspGluValValValThrAsnAsnProAlaGlyGlyIleSerAlaProThrPhe 398
 Db 2828 CGACCAAAAGAGTGTATGATCGAATACCAATGTAATCTGACAAACAGATCGAAT 2887
 QY 399 ThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeu 418
 Db 2888 ACTAGCAAGCACCC-----TTCAAAATCTCACCTTG 2920
 QY 419 GluThrArgProSer---SerArgArgLeuGluLeuPro-----MetProProAlaAsp 435
 Db 2921 AAAAAGGCGCCCAATTGTCAGCTGTGACAGATCCCGACTTATGAAAGACACCA 2980
 QY 436 PheGlyGlnThrValAlaAsnAsnProLysIleGluGlnSerIleuLeuGluTrpLeu 455
 Db 2981 GAAGGAGAAACGACAAATCAATCCA---GTAAATAGTACCTTTGGACAGAGGGGTT 3037
 QY 456 GlyCysTyrIleuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSer 475
 Db 3038 -----CCTTACCAATGCCGCTCTATCGGC 3064
 QY 476 SerPheGlyAlaValSerPhe-----AsnAsnProGlyTyrGluArgThr 490
 Db 3065 AAAAAGTTTCAAGTCTTCACTCGGCAACAGGAAACCAACCAACTGTTTGAAA 3124

QY 491 ArgAspLeuProAspTyrThrGlyIleArgAspSerPheAspGlnAsnMetSerTrpAla 510
 Db 3125 GCAGAGTGTACTATTTGGTGTATTAAGATAGTACGTGATTAACCTTC----- 3175
 QY 511 ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrIleThrTyrGlnGly 530
 Db 3176 -----GTGAGATTCGTCCCAATGATCAAGAGTGTGTACACCAACAGCAGCAAGGC 3226
 QY 531 TrpGluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAlaGlyLeuLeu 550
 Db 3227 TTCATCAGTGTGCCAAGCTTCGAC-----TTGCGCAAGTGGCGCTGCAGGAACTAAG 3280
 QY 551 LysAsnGluGlnIleLeuCysLeuAlaAsp----- 560
 Db 3281 CAACACACAGCTTGAACACAGCCGGATTAACAGGTACAGCGCACAGGAATCCGTAT 3340
 QY 561 -----AspLeuAlaThrArgLeuThrGlyValTyr 570
 Db 3341 CTGCGGATTTAAGAAACGCAACCAATGGAGCTTAAACAGCCGACTGTCAACCAAAA 3400
 QY 571 ProAlaThrAspAsnPhe-----AlaAlaAlaValSer 581
 Db 3401 TCAGCGACACAGACCTTGCTCTACAGCAGCCGCTTATTAAGGGCGGCTGTCTCT 3460
 QY 582 AlaPheAlaAlaAsnMetLeuSerSerValIleuLysSerGlu-----AlaThrSerSer 599
 Db 3461 AGCTTACCAATTACATCAACCAACGAGTTAAAAATAGCGTCCGTACACGAGATGCC 3520
 QY 600 IleIleLysSerValGlyGlnTrpAla 608
 Db 3521 ATTAGCTTACAGCCAAACACACAGCA 3547

RESULT 7

US-09-071-035-417
 ; Sequence 417, Application US/09071035
 ; Patent No. 6448043
 ; GENERAL INFORMATION:
 ; APPLICANT: Gil H. Choi
 ; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 ; NUMBER OF SEQUENCES: 496
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/071,035
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: A. Anders Brookes
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PB369P2.
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 417:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3840 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 US-09-071-035-417

Alignment Scores:

Pred. No.: 0.000329 Length: 3840
 Score: 139.50 Matches: 140
 Percent Simlarity: 31.38% Conservative: 95
 Best Local Similarity: 18.69% Mismatches: 247
 Query Match: 4.13% Indels: 267
 DB: 4 Gaps: 31

US-09-677-653a-50 (1-647) x US-09-071-035-417 (1-3840)

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Oy 19 AsnValArgValSerAlaAsnThrValThrValAsnGlyArgArgAsnGlnArgArg 38
Db 1762 AACCCCAAGTCCAGAGAACTTCGTAGACACACAGCGCGCTAA----- 1806

Oy 39 ThrGlyArgGlnValSerProProAspAsnPhetThrAlaAlaGlnAspLeuAlaGln 58
Db 1807 -----ATCACACCGCCCAACAGCTTCCACCCCAAGTAAACGCGTATTACA 1854

Oy 59 SerLeuAspAlaAsnThrVal-----ThrPheProAlaAsnIleSerSer--- 73
Db 1855 AGC-----GACGCTTACACTTTCAAACAGACAGCAGCAGCTTACACAGACTTACACAGCG 1911

Oy 74 -----MetProGluPheArgAsnThrAlaLysGlyLysIleAspLeuAspSerAspSer 91
Db 1912 GGTAAAGCTACACAGTTCACAAAGCTTGTCACAAAGCCAGCATCCATCTCAACACATTGACA 1971

Oy 92 IleGlyTrpThrPheLysThrLeuAspProAlaGlyAlaThrGluSerIleArgIleVal 111
Db 1972 ACT----- 1974

Oy 112 GlyIleuTrpSerLysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArg 131
Db 1975 -----ACCAAAAGCCGCAAGTATATCAAGTACCTACAGATGACATGATGATTTGAAT 2025

Oy 132 GluIleuTrpAsnGluGlyCysProValValThrAspValSerValProLeuAsp----- 149
Db 2026 GTGGGTATGAAGAAAGAACACGTTACGACAGTATCCATCGATGATGAACTTTGCG 2085

Oy 150 -----GlyArgGlnIlePheSerLeu 155
Db 2086 AATGAAAAGGCGGCGCTTTCACACCGCGCTTAAGTTCAGTGGTAACTATATGCGCAA 2145

Oy 156 SerIlePheSerPheProMetPheArgThrAlaTrpValAlaValAlaAsnValGluAsn 175
Db 2146 AGTACGAGTGCCTAC-----TTAAGAACCGCATTTATATGACGTGCCTCAAAAATATAT 2199

Oy 176 -----LysGluMetSerLeuAspValValAsnAspLeu 186
Db 2200 GGTAATGGCAATATACGGTAAGTATTAATAATGGTAGTATGCATTTGCCAAGAAATTA 2259

Oy 187 IleGluTrpLeuAsn----- 191
Db 2260 TTGAATAAAATATATATATGACACCAATCAAGTCTACACACAGATTTAATGTT 2319

Oy 191 ----- 191
Db 2320 GATAAATTAGCATGACCAACAACTAAATATGTTGACAGCATTCATTAAGACACAGCT 2379

Oy 192 -----AsnLeuAlaAspTrpArgTrpValVal----- 200
Db 2380 CAAGTACCAATCTGAAATTCCTATGATATATGTACAGAACAAATAGCTCACTGTTTTC 2439

Oy 201 -----AspSerGluGlnIlePheLeu 207
Db 2440 GACCAAAATGTAAGCACACAGAGTTCAGCTTACTTACAGAAATCTTAACTTGCCTAAT 2499

Oy 208 PheThrAsnAspThrThrTyTrp----- 215
Db 2500 TTGTGATTAGATGACACTATTTTCTAATGCAAAATATAGACTTTTTCACGCAATTA 2559

Oy 216 -----ValArgIleArgValIleuArgProThrTyTrpAspVal--- 227

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Db 2560 GGATATAGTGGCACACACAGAGTTAACTATCTTCGTGAATGTTCTTTTAACGCCAA 2619

Oy 228 ProAspProThrGluGlyLeuValArgThrValSerAspTrpArgLeuThrTyTrpAla 247
Db 2620 CCTGGCGATTAAGTCAAAACTTGTTC-----TACAAAGTCTCTGCAAAACAA 2664

Oy 248 IleThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGln 267
Db 2665 GTACAC-----GAAAACCTCGTGAT-----GTCAACGCTGCC 2697

Oy 268 TyrAlaLeuThrProThrSerLeuProGlnIleTyTrpAspValSerGluAlaTrpAlaLeuHis 287
Db 2698 AAAATCATCTGACCAACAGCTTACACCA-----GTAAACCAAGTACCAATGAAC 2748

Oy 288 ThrLeuThrPheAlaArgProSerSerAlaAlaAlaLeu----- 300
Db 2749 AGTACACCTTC-----AAGTACACAGCGGCAAAAGCTTTTACACGACGATATCTACAGGT 2805

Oy 301 -----AlaPheValTrpAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrPro 318
Db 2806 GGCAAAAGTCTATACGTTCCAAAGGTGTGTAAAGGAAACCAAGCAAGTACGTTG--- 2862

Oy 319 AlaTrpGluGlnAlaSerSerGlyGlyLeuThrTrpArgHisAsnGlyThrThrPhe 338
Db 2863 -----AACAAACCAACACT 2877

Oy 339 ProAlaGlySerValSerTrpValLeuProGlnGlyPheAlaLeuGluTrpArgPro 358
Db 2878 CCAAGCTTAATGCGAC-----TTGATGCGC 2904

Oy 359 AsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnVal 378
Db 2905 AATGACGATATACCGCGCATGTATGAAGAAATACCAACAGTAGTGTCACTTAAT 2964

Oy 379 AlaValAspGluValValValThrAsnAsnProAlaGlyGlyGlySerAlaProThrPhe 398
Db 2965 CGACCAAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3024

Oy 399 ThrValArgValProProSerAsnAlaTrpThrAsnThrValPheArgAsnThrLeuLeu 418
Db 3025 ACTACCAAAAGCACCC-----TTTCAAAATCTACCTTG 3057

Oy 419 GluThrArgProSer-----SerArgArgLeuGluLeuPro-----MetProProAlaAsp 435
Db 3058 AAAAAGGCGCCCAATGTGTCACAGTCTGTCAGATGCCGACCTTATGAAATGACACCA 3117

Oy 436 PheGlyGlnThrValAlaAsnAsnProLysIleGluGlnSerLeuLeuLysGluThrLeu 455
Db 3118 GAAGGAGAAACGACAAATCAATCCCA--GTAAATAGTACACTTGGACAGAGGGGTT 3174

Oy 456 GlyCysTyrLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProLaser 475
Db 3175 -----CCTTACCAAAATCGGCTCTATGCGC 3201

Oy 476 SerPheGlyAlaValSerPhe-----AsnAsnProGlyTyTrpGluArgThr 490
Db 3202 AAAAAGTTCAGTTCCTTCAACAACGCGCAACAGGAAACCAACACTGTTTGA 3261

Oy 491 ArgAspLeuProAspTrpThrGlyIleArgAspSerPheAspGlnAspMetSerThrAla 510
Db 3262 GCAGAGTGTGATATGTTGGTGTATTAACATGTATACAGTGCATGATCTC----- 3312

Oy 511 ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrThrTyTrpGlnGly 530
Db 5111 -----GTAGAAATTCGTTCCAAATGATCAAGAAAGTATGACACCAAGCAAGGCGC 3363

Oy 531 TrpGluGlyValThrAsnValAsnThrProPheGluGlnPheAlaHisAlaGlyLeuLeu 550
Db 3364 TTCATCAGATGTCACCAACTTCGAC-----TTCGSCAAAGTGGCGGTTCAGAGAACTAAG 3417

Oy 551 LysAsnGluGluIleLeuCysLeuAlaAsp----- 560
Db 3418 CAACAAACAGAGCTTGAACACACCGCGGATTTACTAGCGTAAACGACAGCAAGAAATCCGAT 3477

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QY 561 -----AspleuAlaThrArgLeuThnglyValTyr 570
Db 3478 CTGGCGATTAGAAACGCAACCAATTGGAGCTTAACAGCGCACTGTACAAACAAA 3537
QY 571 ProAlaThrAspAspPhe-----AlaAlaAlaValSer 581
Db 3538 TCAGCGACAGACAGCTTGCTTACAGCGACCGCTTATTATTAAGGGGGCGCTGTCT 3597
QY 582 AlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerLys-----AlaThrSerSer 599
Db 3598 AGCTTTACCAATTACATTCACACCAACCGAGCTGAAATAATACGGTGTACACGAGTGCC 3657
QY 600 IleIleLysSerValGlyLysThrAla 608
Db 3658 ATTAGCTTAACAGCAACCAACACGACA 3684

RESULT 8
US-09-199-290-33
; Sequence 33, Application US/09199290
; Patient No. 6255084
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne R.
; APPLICANT: Nielsen, Ruby
; APPLICANT: Lehmebeck, Jan
; TITLE OF INVENTION: Thermostable Glucoamylase
; FILE REFERENCE: 5279,200-US
; CURRENT APPLICATION NUMBER: US/09/199,290
; EARLIER FILING DATE: 1998-11-24
; EARLIER APPLICATION NUMBER: 1557/97
; EARLIER FILING DATE: 1997-12-30
; EARLIER APPLICATION NUMBER: 0925/98
; EARLIER FILING DATE: 1998-07-10
; EARLIER APPLICATION NUMBER: 60/070,746
; EARLIER FILING DATE: 1998-01-08
; EARLIER APPLICATION NUMBER: 60/094,344
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/979,673
; EARLIER FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 09/107,657
; EARLIER FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: Talaromyces emersonii
US-09-199-290-33

Alignment Scores:
Pred. No.: 0.0057 Length: 2748
Score: 125.50 Matches: 103
Percent Similarity: 31.94% Conservative: 58
Best Local Similarity: 20.44% Mismatches: 182
Query Match: 3.72% Indels: 161
DB: 4 Gaps: 23

US-09-677-653a-50 (1-647) x US-09-199-290-33 (1-2748)
QY 40 G1YArgGlnValSerProAspAsn----- 48
Db 1370 GGTAGCGAATGATATATTCGCGACAGCGGTGACTAATTTGATTCAGACCTCTGGGAA 1429
QY 49 -----PheThrAlaAlaAlaGlnAspLeuAlaGlnSerLeuAsp 61
Db 1430 GAAGTAGAAGATCCATCTTCATTCACAAACCGCGTGCACACACCGCGCC---CTGGTGA 1486
QY 62 AlaAsnThrValThrPheProAlaAsn-----IleSerSerMetPro 75
Db 1487 GGCATTCACCTGGCAGACAGGCTGAGACACACGCTCTCAACGCTGCTCAGGCCCT 1546
QY 76 GluPhe-----ArgAsnTrp----- 80

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Db 1547 CAGGTCCCTGTCTTCTCGCATCATGACTGACCGGATCGTATGTTCTGCCAACTTTGCT 1606
QY 81 AlAlaYsGlyLysIleAspLeuAspSerAspSerIleGlyTrpThrPheLysThrLeuAsp 100
Db 1607 GGCAGCGGTCTCTCCGCAAGAGAGAGATTCGATTCGTGGGACATCATCACACCTTTGAT 1666
QY 101 ProAlaGlyAlaThrGlu-----SerAlaArgAlaValGlyLys 113
Db 1667 CCGCCCGGAGGCTGTGACGACGCTGACCTTCACAGCCGTGTCGCGCCCTGGCTGGCAAT 1726
QY 114 TyrSerLysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArgGluIle 133
Db 1727 CACAAGGTGTGACACCGAC-----TCGTTCCGAGATATC 1759
QY 134 TyrAsnGluGlyLysProValValThrAspValSerValProLeuAspGlyArg----- 151
Db 1760 TATGCGATCAACTCAGCATCGACATCGAGAGGATGTGCGTGGCAGATC---GGCCGCTAC 1816
QY 151 ----- 151
Db 1817 GAGGATCTTACACAGGCGGGAACCCCTGTACTGGCCACAGAGCGGCTGCAGACAG 1876
QY 152 -----GlnTrp-----SerLeuSerIlePheSer 159
Db 1877 CTTTACGACGCGCATCTACCATGAGAGAGATCGCTCGATTAAGTATCAGGAGAGCTTAGT 1936
QY 160 PheProMetPheArgThrAlaTyrValAlaValAlaAsnValGluAsnLysGluMetSer 179
Db 1937 CTGCGATTTTCCAGGATATCATCTCCCTGCGCCG---GTGGCAGCATTAATCTGAGC 1993
QY 180 LeuAspValValAsnAspLeuIleGluTrpLeuAsnMetLeuAlaAspTrp----- 196
Db 1994 TCACGACTTTCACGACATCATCTCGCCGCTGCACAGCATGATGATGATATCTGAGT 2053
QY 197 -----ArgTyrValValAspSerGlu-----GlnTrp-IleAsnPheThr 209
Db 2054 ATTGCTGACGTTTGGCTGTGATTCAGAGTGAAGAAAAAATGAACTAATCAGT 2113
QY 209 PAsnAspThrThrTyrTyrValArgIleArgValLeuArgProThrTyrAspValProAs 229
Db 2114 TCTAGGAAATATATCTCCCTCAG-----CGGCTCTTACGAAACATTTCT 2161
QY 229 Pro-ThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyrLysAla---I 248
Db 2162 CCGTACAGAGCGGACCTCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2221
QY 248 IeThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGlnTr 268
Db 2222 TAACCGCTTGGCGCGGAGACAGTCCGTCGTC----- 2253
QY 268 YrAlaLeuThrProThrSerLeuProGlnTyrAspValSerGluAlaTyrAlaLeuHisT 288
Db 2254 -----CCGTCTCTCGGGGCGAAGCTCCGCAAGAGCGTCCCTGCTGCTGCT 2302
QY 288 hrLeuThrPheAlaArgProSerSerAlaAlaAlaLeuAlaPheValThrAlaGlyLeuP 308
Db 2303 CTGCCACCTTGCACAGGCGCCCATATACAGACGCTACCAACACCGTGTGGCAAGCTCTG 2362
QY 308 roGlnGly-----GlyThrAlaProAlaGlyThrProAlaTrpLysGln 323
Db 2363 GCTGTGACAGCTCAACACACAGCTAGCGGCCCATGACACACCTCTGCTGCTGCTGCTGCT 2422
QY 323 IAspSerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrThrPheProAlaGlySerV 343
Db 2423 TGACCTTCGAGGAATGTCAGCACCAAGTATACGGGAGGAGCAATCTACTGCGCGCTCGA 2482
QY 343 aIleSerTyrValLeuProGluGlyPheAlaLeuGluIleArgTyrAspProAsnAspLys 363
Db 2483 TC-----CCGAGCTGGGCACT 2500
QY 363 rPThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaValAspLys 383
Db 2501 GG-----TCCAGCGGCGAGCGGATCCCGCTCGGGCG-----GATG 2536

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QY 383 aValValThrAsnAsnProAlaGlyGlySerAlaProThrPheThrValArgValP 403
DB 2537 CTACACCAACGACACCGCTCTGG-----TACGACCGCTCAATCTGC 2581
QY 403 roProSerAsnAlaTyrThrAsnThrValPheArgAsn-----ThrLeuG 419
DB 2582 CCCCTGGCACAGCTTCGAGTACAAAGTCTCTCAAGAACGACGAGGAGCCATCGTCT 2641
QY 419 luthrArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnT 439
DB 2642 GGGAGACGACACCGGACCGGTCTGCTACACGCTC-----CCAGGCTACTGTGGCAGA 2692
QY 439 hrValAla 441
DB 2693 CTACCGCC 2700

RESULT 9
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Alignment Scores:
Pred. No.: 2.4e+03 Length: 4403765
Score: 124.00 Matches: 169
Best Local Similarity: 30.968 Conservative: 74
Similarity: 21.538 Mismatches: 280
Query Match: 3.688 Indels: 263
DB: 4 Gaps: 39

US-09-677-653A-50 (1-647) x US-09-103-840A-2 (1-4403765)
QY 9 GluAlaProHisAsnArgArg-----GlyThrArgAsnVal---ArgVal 22
DB 3373909 CGCCAAACCCGACCGCGCTGCACACGACGACCCGAAACGACGATACGTACGCGACA 3373968
QY 23 SerAlaAsnThrValThrValAsnGlyArgArg-----AsnGlnArg 36
DB 3373969 CGGAATCTGACCGCGGTGGGAGGACACCGGATCACCGGTAGCGGAATCATGTGGGG 3374028
QY 37 ArgArgThrGlyArgGlnValSerProProAspAsnPhe----- 49
DB 3374029 CGGCGACCGCGGTGCGTCAACGCTTCACCGCGGACGTGGCGCCGCAACCCCTCAGGAA 3374088
QY 50 -----ThrAlaAlaGln 54
DB 3374089 CCACGCTCAGGCTCACGACGACACTCTTCCTTAGCGCGCTCCACACACCATCTCCCGG 3374148
QY 55 AspLeuAlaGlnSerLeuAspAlaAsnThrValThrPhePro-----Ala 69
DB 3374149 ATTTTGCTCTATCAAGCTGTGTAAATAGCTACGATTCACGAGCGGTAGACGACGACGCC 3374208

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QY 70 AsnIleSerSerMetProGluPheArgAsnTrp----- 80
DB 3374209 GCAAGATTCCTCACACCCCGCGCTGGCAATTGGCCACGACGACCGCGGACGAGGCC 3374268
QY 81 -----AlaGlyGlyLysIleAspLeuAsp 88
DB 3374269 GCCACGCCACACCAAGCTCTCGCCGACCAACATCGCGCTACCGGATCCACCAAC--AGC 3374325
QY 89 SerAspSerIleGlyTrp---TyrPheLysTyrLeuAspProAlaGlyAlaThrGlnSer 107
DB 3374326 GCACGGCATTTGGATGGGGGCCCATCAACCCAGCATCATCCGGCGTGGCCGACACAC 3374385
QY 108 AlaArgAlaValGlyLysTyrSerLysIleProAspGlyLeuValLysPheSerValAsp 127
DB 3374386 GCCCGCGCGCTG----- 3374397
QY 128 AlaGluIleArgGluIleTyrAsnGluGlyCys---ProValValThrAspAlaSerVal 146
DB 3374398 -----TCTTAGCGCGCCCTTGGCGCTTGGCC 3374427
QY 147 ProLeuAspGlyArgGlnTrpSerLeuSerIlePheSerPheProMetPheArgThrAla 166
DB 3374428 CCA----- 3374430
QY 167 TyrValAlaValAlaAsnValGluAsnLysGluMetSerLeuAspValAlaAsnAspLeu 186
DB 3374431 -----TCTCGACGCAACATC-----GCCATGCTTGGAC----- 3374460
QY 187 IleGluTrpLeuAsnAsnLeuAlaAspTrpArgTyrValValAspSerGluGlnTrpIle 206
DB 3374461 --TCATGGGTGCCAGACATGACATGATAGGCGCCGACAGATCTCTAGGCGCTGCTC 3374517
QY 207 AspPheThrAsnAspThrThrTyrTyrValArgIleArgValLeuLeuProThrTyrAsp 226
DB 3374518 CACTGG-----GTCGTCACCGCTGATACGTCG 3374544
QY 227 ValPro---AspProThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyr 245
DB 3374545 ATCCGGATATGACACCTCGCAAGCACTGGACAGACGACGCGCTGCTACGCGATATCGGCC 3374604
QY 246 LysAlaIleThrCysGluAlaAsnMetProThrIleValAlaAspGlnGlyPheTrpIleGly 265
DB 3374605 CCCAAGCTCTCGAAGCGTCCCGGACATACCGGACATGCTCCCGGACATGAGCATCTGCC 3374664
QY 266 Gly---GluTyrAlaLeuThrProThrSerLeuProGlnTyrAspValSerGluAlaTyr 284
DB 3374665 GGATAGTGTGTACATATATGTC-----GACATCAACAACCCCTTT 3374703
QY 285 AlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAlaAlaLeuAlaPheValTrp 304
DB 3374704 TCATTCGAGGACGACATTTTAAACCCGCTGATGCTGGACGC-----GGC 3374751
QY 305 AlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrpGluAlaSer 324
DB 3374752 GCGCGCATCTCG--CGGCGCAATACGTCGCGCGGCTCCCAAAATGGCTTGGCGGATAT 3374810
QY 325 SerGlyGlyTyrLeuThrPheArg-----HisAsnGlyThr 336
DB 3374811 CCAGCAAGGTATGACCTTGGGCGCGCGGCGGACCAACCGGCGCATGCGCCATGAAACG 3374870
QY 337 -----ThrPheProAlaGly----- 341
DB 3374871 CCGCGCGGACTCTCCCTGATGAACAGCTCGCGCGACATGCGCTGCTGCTGGCTGAC 3374930
QY 341 ----- 341
DB 3374931 CGATGTATGCGCGATCAACCCCGCTTAGCGGAAACGCGGTATGCGAAGCATCAACT 3374990
QY 342 -----SerValSerTyrValLeuProGlnGlyPheAlaLeuGln 354
DB 3374991 GCGGATATGCGGATCCAAACCAATCATCAACATTCCTTCA-----ATTGCAATACCC 3375044
QY 355 ArgTyrAspProAsnAspLysSerTrpThrAspPhe-----AlaSerAlaGlyAsp 371

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Db 3375045 AATTACTCGCGGTAGATGCTCAAA-----ACTGACACCAACCCCATACCGGCGCACACGG 3375101
OY 372 ThrValThrPheAlaGlnVal-----AlaValAspGlu 382
Db 3375102 ACCAAATCCGGCCCCCGACGCTCCCGGAGCATCGGCACCGCGCACCATCATCCAAATCTCA 3375161
OY 383 ValValValThrAsnAsnProAlaGlyGlySerAlaProThrPheThrValAlaGlyVal 402
Db 3375162 TCGGCGCAACACCGGTCAACCCCGCGGC-----TCCCAACCGACTCTTGTCCACGCC 3375212
OY 403 ProProSerAsn-----AlaTyrThrAsnThrValPhe 413
Db 3375213 GTCCCAACCAAAACCCCAACGCCCGCCAGCACCCGATCAGAAACGACGACCGACGACGCGT 3375272
OY 414 ArgAsnThrLeuLeuGluThrArgProSerSerArgAlaGlyLeuLeuProMetProPro 433
Db 3375273 CTGCGCGGAGACCGGCTCCACCGCGGACACCAACCGCGCTGCGGCGACACCAACCGCACCC 3375322
OY 434 AlaAspPheGlyGlnThrValAlaAsnAsnProHysIleGlnIleSerLeuLeuGlu 453
Db 3375323 ---GACACCGCGCGCACACATGCGCCACCAAC-----CGCGCGGCGGCGGACAGCGCGCACCC 3375386
OY 454 ThrLeuGlyCysTyrLeuValHisSerLysMetArgAsnProValPheGlnLeuThrPro 473
Db 3375387 ACCGCGCGC-----ACAGCGCGCAACCCCGCCCAACCCCGTCACACCAACCGCACCC 3375437
OY 474 AlaSerSerPheGlyAlaValSerPheAsnAsnProGlyTyrGluArgThrArgAspLeu 493
Db 3375438 GGCACACCGCGACAGCGCAACGCCGCCCAACACGGA----- 3375473
OY 494 ProAspTyrThrGlyTleArgAspSerPheAspGlnAsnMetSerThrAlaValAlaHis 513
Db 3375474 CCGCGCAAAACCGGAATA-----GCGCAAAATA 3375503
OY 514 PheArgSerLeuSerHisSerCysSerLeuVal---ThrLysThrTyrGlnGlyTyrGlu 532
Db 3375504 TTGCAAAATTAATCCACCAACCAATCTGAGTATCGCCAGTCCAAAGACCAACCGCAATTCTAAT 3375563
OY 533 GlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAlaGlyLeuLeuLysAsn 552
Db 3375564 AGCGGACCGCAACCAATACGCT-----AACGCAAAACCTACCGGCGGCAAAAC 3375614
OY 553 GluGluIleLeuCysLeuAlaAspAspLeuAlaThrArgLeuThr---GlyValTyrPro 571
Db 3375615 ATATCGATCTATCCCGGTAAGAGACGACCAAGCTCGAAATTTACACAGACCGCGTATCAGC 3375674
OY 572 AlaThrAspAsnPheAlaAlaAlaValSerAlaPheAlaAlaAsnMetLeuSerSerVal 591
Db 3375675 TCGACGAATCCCAACGCCAGCGCTGCGGCTCTTCAATTCAATTTGCGGACCTCGTA 3375734
OY 592 LeuLysSerGluAlaThrSerSerIleLeuLysSerValGlyGluThr----- 607
Db 3375735 -----AATCTGGGAGGACCATTTCCAAAACCTTCGTAATTCGCAATGGGAAT 3375785
OY 608 -----AlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeu---ProGlyLeuMetMet 624
Db 3375786 GGGGTTATAGTTGGCGGCGGCGACAGGCGCTTCGCTTCATTTGATGCGCGCGGTGGAGATG 3375845
OY 625 Ser-ValProGlyLysIleAlaAlaArgValAlaArgValAlaArg-----AlaArgArg 641
Db 3375846 ACCGCGTCCGCGCGCGGTGTGTGTGGCCACACGACGCGCACCAACCGACCGCTATAG 3375905
OY 641 GARGAlaAlaArg 645
Db 3375906 GCGCTCATCAACGG 3375918

RESULT 10
US-08-917-320-18
: Sequence 18, Application US/08917320
: Patent No. 5824508
: GENERAL INFORMATION:
: APPLICANT: Spaeete, Richard and Jackman, Winthrop, T.

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[illegible]

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Db 1767 GCCACC-----CCAATACCTGGTACAGGGTATGCATACAGCCCTGGCTGACACCAGCT 1820
Qy 161 Promethylpharyg-----ThralatyrValAlaValAlaasnValglu 174
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Db 1821 CCAGGTGTACAGATTTCTTGGCATAACAGTATCCTGTAGTGTTCAGCTGGGATGGA 1880
Qy 175 AsnLysGluMetSerLeuasp-----ValValasnAspLeuile 187
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Db 1881 CCGAAGCGGAGCGGGGAGATTTACTGCATTCAGTCCACATTTGTCTGTCTGTAGAT 1940
Qy 188 -----GluTrpLeuasnInleuAlaAspTrpArgTyrTyrValAlaAspSerGlu 203
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Db 1941 CCAGCTTCACAGGATGCCCGCAAAACACACACATGATGATGGTGCAAT--- 1997
Qy 204 GluTrpLeasnPhethrasnAspThrTyrTyrValArgIleargValLeuArgPro 223
Db 1998 -----GCT 2000
Qy 224 ThrTyrAspValProAspProThrGluGluValArgThrValSerAspTyrArgLeu 243
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b 2001 ACCGATTCAGTCCAAATGGTCACTCTGAG----- 2030
Qy 244 ThrTyrLysAlaIlethrcysGluAlaasnMetProThrLeuValAspGlnGlyPheTrp 263
Db 2031 -----GACGCAAACTGCGCAAAATGTTACAGTGCCTGCTTTGG 2069
Qy 263 ----- 263
Db 2070 GCGTGGCCAAACACATGAACCTTAAGTGAATGAGACCTCAGCTGGGAGCA 2129
Qy 264 -----IleGlyGlnTyrAlaLeuThrProThr----- 273
Db 2130 CCTTGGGTTGTGAAATATTTCTGTGATTTGGGAGCAATGCGACATTTGACATTACT 2189
Qy 273 ----- 273
Db 2190 GTCTGGGCTTGGGACGGCCCAAGACATCATTTATTCACAGCAAGCGCTACCAATGCC 2249
Qy 274 -----SerLeuProGlnTyrAspValSerGluAlaTyr 284
Db 2250 ACCACACACACCCACATGTTATTTCTCAAGGACCCGGAAGACACCCACCTCCCT 2309
Qy 285 AlaLeuHisThrLeuThrPheAlaArgProSerSerAlaIleAlaLeuAlaPheValTrp 304
   ||||| |||||
Db 2310 ACCTTGATATACAACTGATTTCTGATCCCAATACACG----- 2348
Qy 305 AlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrpGlnAlaSer 324
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Db 2349 ACAGGTCTACCCAGCTCTACTACGTGCTTACCAACCTCACCGCA-----CCTCCAAAC 2402
Qy 325 SerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrThrPheProAlaGlySerValSer 344
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Db 2403 ACAGGCCCCACGTATCCACCGCGGATGTACACACCCCAACACGCGGCAACAGTCA 2462
Qy 345 TyrValLeuProGlnGlyPheAlaLeuGluArgTyrAspProAsnAspGlySerTrp--- 363
   ||||| |||||
Db 2463 GCGCGATCACCG-----GTGACACCAAGTCCATCTCATGGGAC 2501
Qy 364 -----ThraspPheAlaSerAlaGlyAspThrValThrhe--- 375
Db 2502 AACGGCAGAGAAAGTAGAGCCCGCCGACATGACACCTCCACCTCCACGACCTACCCCA 2561
Qy 376 ArgGlnValAlaValAspGluValAlaValThrAsnAsnProAlaGlyGlySerAla 395
   ||||| |||||
Db 2562 ACCCAAAATGCCACACAGCCCGCCACGACGAGTACCCCAACCCCAATGCCACACAGC 2621
Qy 396 ProThrPheThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsn 415
   ||||| |||||
Db 2622 CCCACCCAGAGTACTACCCCAACCCCAATGCCACACAGC-----CCC 2666
Qy 416 ThrLeuLeuGluThrArgProSerSerArgLeuGluLeuProMetProProAlaAsp 435
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Db 2667 ACCTTGGGAAAAACAAATCTCACTCA-----GCAGTACTACCCCAACCCCAATGCC--- 2720

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Qy 436 PheGlyGlnThrValAlaAsnAsnProLysIleGluInSerLeuLeuysGluThrLeu 455
Db 2721 -----ACGACCCCGACCTTG 2735
Qy 456 GlyCysTyrLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSer 475
   ||||| |||||
Db 2736 GGAAMAAACAGCCCGCCACCTCACAGTCACTACCCCA-----ACCCCAATGCC 2783
Qy 476 SerPheGlyAlaValSerPheAsnAsnProGlyTyrGluArgThrArgAspLeuProAsp 495
   ||||| |||||
Db 2784 ACCAGCCCGCCCTTGGAAMAAACAGCCCGCCACGAGTACGATCCCAACCCCAAT 2843
Qy 496 TyrThrGlyIleArgAspSerPheAsnGlnAsnMetSerThrAlaValAlaHisPheArg 515
   ||||| |||||
Db 2844 GGCACCGCCCGCTACGTGGGAGAAACAACTCCACAGGCAAAATGCCACACACACCTTA 2903
Qy 516 SerLeuSerHisSerCysSerIleValThrLys-----Thr 527
   ||||| |||||
Db 2904 GAGAGCAACAGTCCCGCCACCCAGTACGATACAGCCAAACAAATGCAACAGTCTGT 2963
Qy 528 TyrGlnGlyTrpGluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAla 547
Db 2964 ACCACAGGCCCAACATPACATPACATTCAGTCAAGTCAACCTTCCATGTCAGTCAAGACCCAGT 3023
Qy 548 GlyLeuLeuLysAsnGluGluIleLeu-----CysLeuAlaAspAspLeuAlaThrArg 565
Db 3024 -----TCAACCCAGAGACACTCAGCCCTCCACAGTACATTCACAGTCACT 3074
Qy 566 -----LeuThrGlyValThrProAla-----ThrAsnAsnPheAla 577
Db 3075 ATGCTTTTACTAATCCCTCCCTCACCCACAGGTGTGAAATATPATAACAGGTGACACA 3134
Qy 578 AlaAlaValSerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerLysAlaThr 597
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Db 3135 GCGCTATATGACACATCATGTGTCCACAGTGTGCCAGAAACCCGCGGACAGCCACAC 3194
Qy 598 SerSerIleIleLysSerValGlyGluThrAlaValAlaAlaGlnSerGlyLeuAla 617
   ||||| |||||
Db 3195 AGCCAA-----GGCTAGGCGCCGGAACAGTCCACATCC 3230
Qy 618 LysLeuPro-GlyLeuLeuMetSerVal-----ProGlyLysIleAlaAlaArgVa 634
   ||||| |||||
Db 3231 ACMAAACCGGGGAGGTATATTCACAAAGGACAGCCCGCCCAAAATGCAACAGTCCGCC 3290
Qy 634 ArgAlaArgArgAlaArgArgArg 642
Db 3291 CAGGCCCGCCAGTGGCCAAAGACGG 3315

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RESULT 11
 PCT-US95-04611A-18
 ; Sequence 18, Application PC/US9504611A
 ; GENERAL INFORMATION:
 ; APPLICANT: Spate, Richard and Jackman, Winthrop, T.
 ; TITLE OF INVENTION: Non Splicing Variants of gp350/220
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 ; STREET: 5 Palo Alto Square
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/04611A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:

Db 2904 GGAGGACAAAGTCCACCCCAAGTACTACACGCAACCAAAAAATGCAACACAGTCTGTT 2963
Oy 528 TGTGNGLTTPRGLUGLYVALThrasnValAsnthrProphGlyGlnPheAlaHisAla 547
Db 2964 ACCACAGCGCAACATACATTAAGTTCACAGTCAACCTCTTCATCTCACTGAGACCCAGT 3023
Oy 548 GlyLeuLeuLysAsnGluGluLeuLeu-----CysLeuAlaAspSpleuAlaThrArg 565
Db 3024 -----TCAACCCAGACACTCAAGCCCTCCACACAGTACAAATTCACACGTCACAT 3074
Oy 566 -----LeuThrGlyValTyProAla-----ThraspAsnPhlea 577
Db 3075 ATGCTTACTACCTCCGCTCACCACAGGTGTAATAATATACACAGGTGACACCA 3134
Oy 578 AlaAlaValSerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThr 597
Db 3135 GCCTTATACGACACATCATGTGTCCACAGTTCGCCAGAACCCGCCACGACACACCC 3194
Oy 598 SerSerIleIleLysSerValGlyGlnThraValAlaGlyAlaGlnSerGlyLeuAla 617
Db 3195 AGCCAA-----GGTCAAGGCCCTGGAAACAGTTCACATCC 3230
Oy 618 LysLeuPro-GlyLeuLeuMetSerVal-----ProGlyLysIleAlaAlaLysVal 634
Db 3231 ACAAAACCGGGAGGTTAATGTCCACAAAGGACGACGCCCCCAAAATATGCAACGTGCC 3290
Oy 634 LArgAlaArgAlaArgAlaArgArg 642
Db 3291 CAGGCCCCCACTGGCCAAAGACGG 3315

RESULT 12
US-08-783-774-1
Sequence 1, Application US/08783774
Patent No. 6054130
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
TITLE OF INVENTION: Jackman, Winthrop
TITLE OF INVENTION: NON-SPLICING VARIANTS OF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,774
FILING DATE: 15-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-0900
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5931 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:

/ NAME/KEY: Coding Sequence
/ LOCATION: 1014...3734
/ OTHER INFORMATION:
US-08-783-774-1

Alignment Scores:
Pred. No.: 0.0636 Length: 5931
Score: 121.00 Matches: 145
Percent Similarity: 30.18% Conservative: 69
Best Local Similarity: 20.45% Mismatches: 272
Query Match: 3.59% Indels: 223
Gaps: 30

US-09-677-653A-50 (1-647) x US-08-783-774-1 (1-5931)

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Db 1518 AATATACGGGCGAGTAGTGG-----GCACAGGGGGCTGAGT-----GTCACGCTA 1562
Oy 68 ProAlaAsnIleSerSerMetProGluPheArgAsnthrPalalysGlyLysIleAspLeu 87
Db 1563 CCCTTAAGTTGCCAAGCTCAGCTCAGACTCGAATTCACG-----GTA 1607
Oy 88 AspSerAspSerIleGlyTrpTyProLysTyLeuAspProAlaGlyAlaThrGluSer 107
Db 1608 AAACAGAAATGCTCGT-----AATGAGATAGAT-----ATTGAGTGT 1646
Oy 108 AlaArgAlaValGlyGluTySerLysIleProAspGlyLeuValLysPheSerValAsp 127
Db 1647 ATTATGAGAGATGGGCAATTCACAGTTCGCCGAGACACAAATTTAACTACACC 1706
Oy 128 AlaGluIleArgGlu-----IleTyAsnGluGluCysProVal 140
Db 1707 TGCACTGATACGACAGGATGTTCCACGGGCGAATTCACATCAACGAGTCCGCTG 1766
Oy 141 ValThrAspValSerValProLeuAspGlyArgGlnTrpSerLeuSerIlePheSerPhe 160
Db 1767 GCCACC-----CCAAATACCTGGTACAGGATGATGATGACGCTGCTGACACACAGT 1820
Oy 161 PrometPheArg-----ThraTyValAlaValAlaAsnValGlu 174
Db 1821 CCAGTGTACAGATTTCTTGGCATAATACAGTATCTGTACGTGTTTACTGTGGAGATCGA 1880
Oy 175 AsnLysGluMetSerLeuAsp-----ValValAsnAspLeuIle 187
Db 1881 CCGAAGGGGAGGGGGGAGATTTACTGATCGACCAACATTTGTTCTGATGACATTT 1940
Oy 188 -----GluTrpLeuAsnAsnLeuAlaAspTrpArgTyValValAspSerGlu 203
Db 1941 CCAGCTTCACAGACATCCGACAAACACACACAGACATCATATATGTGGTACAT-- 1997
Oy 204 GlnTrpIleAsnPheThrAsnAspThrThrTyValAlaGlyIleArgValLeuArgPro 223
Db 1998 -----GCT 2000
Oy 224 ThrTyAspValProAspProThrGluGlyLeuValArgThrValSerAspTyArgLeu 243
Db 2001 ACCTATTCAGTCCCAATGTCATCTCTGAG----- 2030
Oy 244 ThrTyLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrp 263
Db 2031 -----GAGCGCAAACTCGCCAAATGTTAACAGTACGCTGCTTTGG 2069
Oy 263 ----- 263
Db 2070 GCCTGGCCAAACACACTGAAACTGACTTTAAGTCAAAATGAGACTCTGCTCGGGGACA 2129
Oy 264 -----IleGlyGlyGlnTyValAlaLeuThrProThr----- 273
Db 2130 CCTTGGGTGTGAATAATATTCTGGTGCATTTGGACACATCGACATTTGACATTACT 2189
Oy 273 ----- 273

Db 2190 GTCTCGGGCTTGGACGGCCCCAGACACTATATTCACAGCAGACGGGTACCAATGCC 2249
QY 274 -----SerLeuProGlnThrValSerGluAlaTyr 284
Db 2250 ACCAACAACCAACCAAGTTATTTCTCCAGGACCCGAGACACCACTCCCT 2309
QY 285 AAlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAlaLeuAlaPheValTyr 304
Db 2310 ACCTGTAAATCAACTGATTTTGGTCGATCCCAATCAACG----- 2348
QY 305 AlagIleuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTyrGluAlaSer 324
Db 2349 ACAGGTCTACCAAGCTTACTCACTGCTCAACCACTCAACGCA-----CTGCAAGC 2402
QY 325 SerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrThrPheProAlaGlySerValSer 344
Db 2403 ACAGGCCCCCTGATATCCACGGGATGTACACGACCCCAACACGCGGACAACTCA 2462
QY 345 TyrValLeuProGlnGlyPheAlaLeuGluArgTyrAspProAsnArgIleSerTrp--- 363
Db 2463 GGGCGCATCACG-----GTGACACCAAGTCATCTCCATGGGAC 2501
QY 364 -----ThrAspPheAlaSerAlaGlyAspThrValThrPhe--- 375
Db 2502 AACGCGACAGAAAGTAAGCCCCGACATGACACGCTCACACGACGATGATACCCCA 2561
QY 376 ArgGlnValAlaValAspGluValValThrAsnAsnProAlaGlyGlyGlySerAla 395
Db 2562 ACCCCAAATGCCACACGCCCCACCCGACGATGATACCCCAATGCCACGAC 2621
QY 396 ProThrPheThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsn 415
Db 2622 CCCACCCGACAGATGATACCCCAACCCCAATGCCACGAC-----CCC 2666
QY 416 ThrLeuLeuGlnThrArgProSerSerArgArgLeuGlnLeuProMetProProAlaAsp 435
Db 2667 ACCTTGGGAAACAACTGCTACTCA---GCAGTACTACCCCAACCCCAATGCC--- 2720
QY 436 PheGlyGlnThrValAlaAsnAsnProGlyIleGluIleSerLeuLeuGluThrLeu 455
Db 2721 -----ACCAGCCCCACCTTG 2735
QY 456 GlyCysThrLeuValHisSerIleMetArgAsnProValPheGlnLeuThrProAlaSer 475
Db 2736 GGAACAAACAGCCCACTGACGATGATACCCCA-----ACCCCAATGCC 2783
QY 476 SerPheGlyAlaValSerPheAsnAsnProGlyTyrGluArgThrArgAspLeuProAsp 495
Db 2784 ACCAGCCCCACCTTGGGAAACAAAGCCCACTGACGATGATACCCCAAT 2843
QY 496 TyrThrGlyIleArgAspSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArg 515
Db 2844 GCCACCGGCTACTGTGGAGAAACAAATGTCACAGCAATGCCCAACCAACCACTTA 2903
QY 516 SerLeuSerHisSerCysSerIleValThrIle-----Thr 527
Db 2904 GGAAGAAACAGTCCCAACCAAGTATTAACAAGCCCAACCAACCAACCAAGTGT 2963
QY 528 TyrGlnGlyTyrGluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAla 547
Db 2964 ACCAAGGCAACATTAACATTAAGTTCAAGTTCCATTCAGTACAGAGCCAGT 3023
QY 548 GlyLeuLeuLysAsnGluIleLeu-----CysLeuAlaAspAspLeuAlaThrArg 565
Db 3024 -----TCAACCCCAAGACACTGACGCCCTCCACAGTGAATTAACCTCAAT 3074
QY 566 -----LeuThrGlyValTyrProAla-----ThrAspAsnPheAla 577
Db 3075 ATGCGTTTACTAATCTCGCTGACCAACAGGTGTGAATAATATACAGGTGACACCA 3134
QY 578 AlaAlaValSerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThr 597
Db 3135 GCGCTATTCAGCAACATCATGTGTCCACAGTTCGCCAAGACCCGCCGAGGACACAC 3194

QY 598 SerSerIleIleLysSerValGlyGluThrAlaValGluAlaGlnSerGlyLeuAla 617
Db 3195 AGCCAA-----GCTGACGCCCCGTGGAACACTTCCACATCC 3230
QY 618 LysLeuPro-GlyLeuLeuMetSerVal-----ProGlyLysIleAlaAlaArgVa 634
Db 3231 ACAAAACGGGGGAGGTATATGTCACCAAAAGGACGCCCCCAAAATGCAAGTGGCCC 3290
QY 634 IArgAlaArgAlaArgArgArg 642
Db 3291 CAGGCCCCCAGGTGGCCAAAGACG 3315
RESULT 13
US-09-556-706B-1
? Sequence 1, Application US/09556706B
? Patent No. 6458364
? GENERAL INFORMATION:
? APPLICANT: Spaele, Richard
? APPLICANT: Jackman, Winthrop
? TITLE OF INVENTION: NON SPLICING VARIANTS OF GP350/220
? FILE REFERENCE: 7682-050-999
? CURRENT APPLICATION NUMBER: US/09/556,706B
? PRIOR FILING DATE: 2000-04-24
? PRIOR APPLICATION NUMBER: 08/783,774
? PRIOR FILING DATE: 1997-01-15
? PRIOR APPLICATION NUMBER: 08/229,291
? NUMBER OF SEQ ID NOS: 19
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 1
? LENGTH: 5931
? TYPE: DNA
? ORGANISM: Virus
? FEATURE:
? OTHER INFORMATION: gp350/220
US-09-556-706B-1
Alignment Scores:
Pred. No.: 0.0636 Length: 5931
Score: 121.00 Matches: 145
Percent Similarity: 30.18% Conservative: 69
Best Local Similarity: 20.45% Misses: 272
Query Match: 3.59% Indels: 223
DB: 4 Gaps: 30
US-09-677-653a-50 (1-647) x US-09-556-706B-1 (1-5931)
QY 48 AsnPheThrAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsnThrValThrPhe 67
Db 1518 AATTAACGGCAGTAGTAGG-----GCACAGGCGCTGAT-----GTCACGCTA 1562
QY 68 ProAlaAsnIleSerSerMetProGluPheArgAsnTrpAlaLysGlyIleAspLeu 87
Db 1563 CCTTAACTTTGCCAAGCTCAAGCTCAAGCTCGAATTTCAAG-----GTA 1607
QY 88 AspSerAspSerIleGlyTyrPheLysTyrIleuAspProAlaGlyAlaThrGluSer 107
Db 1608 AAAACAGAAATGCTCGT-----AATGAGATAGAT-----ATTGAGTGT 1646
QY 108 AlaArgAlaValGlyGluTyrSerLysIleProAspGlyLeuValLysPheSerValAsp 127
Db 1647 AATTAGAGAGATGGCAAAATTTCAAGATTCTGCCGAGACAAACAAATTAACATAC 1706
QY 128 AlagIleuLeuArgIle-----IleTyrAsnGluGluCysProVal 140
Db 1707 TGCAGTGGATACGAGACCATGTTCCAGCGGGGGAATTTCTACATCAACAGATCCCGTG 1766
QY 141 ValThrAspValSerValProLeuAspGlyArgGlnTrpSerLeuSerIlePheSerPhe 160
Db 1767 GCCAC-----CCAATACCTGTGACAGGTATGATCAACAGCTGCTGACACACAGT 1820
QY 161 ProMetThrArg-----ThrAlaTyrValAlaValAlaAsnValGlu 174

Db	1821	CCAGGTCACGATTTCTTGGCAATACAGTATCCTGCTACGTGTTACTCTGGGAATGA	1880
Qy	175	AsnLysgluMetSerLeuAsp-----ValValAsnSpleuIle	187
Db	1881	CCGAAGGCGACGGGGAGATTAATCGCATTCAGTCCACAACTGTGTCTCTCATGATTT	1940
Qy	188	-----GluTrpLeuAsnAsnLeuAlaAspTrpArgTrpValValAsnSerGlu	203
Db	1941	CCAGGTCACAGGACATGCCGACAAACCCACACACATCATCATATGGTGGTCAAT---	1997
Qy	204	GlnTrpIleAsnPheThrAsnAspThrThyTrpValArgIleArgValLeuArgPro	223
Db	1998	-----GCT	2000
Qy	224	ThrTrpAspValProAspProThrGluGlyLeuValArgThrValSerAspTrpArgLeu	243
Db	2001	ACSTATTACAGTGCCAATGGTCACTTGAG-----	2030
Qy	244	ThrTrpLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspGlnGlyHerrp	263
Db	2031	-----GAGCAACTCGCCAAATGTTACAGTGCCTGGCTTTGG	2069
Qy	263	-----	263
Db	2070	GCCTGGCCCAACACACTGAACTGACTTAATGCAATGGACATCTACCTGGGGACA	2129
Qy	264	-----IleGlyGlnTrpAlaLeuThrProThr-----	273
Db	2130	CTTTCGGGTTGTGAAATATTTCTGGTGATTTGGCAGACATTCGGACATTTGACTTACT	2189
Qy	273	-----	273
Db	2190	CTCTCGGGCTTTGGCAGCGCCCCAGACACTATTATACAGCAAGCGGTACCAATGCC	2249
Qy	274	-----SerLeuProGlnTrpAspValSerGluLysr	284
Db	2250	ACCAACACACCCCAAGGTTATATTTCTCCAAAGCACCCGAAAGCACCAACCTCCCT	2309
Qy	285	AlaLeuIsthrIleThrPheAlaArgProSerSerAlaAlaAlaLeuAlaPheValTrp	304
Db	2310	ACSTTGAAATACAACTGGATTGCTGATCCCAATACAG-----	2348
Qy	305	AlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrpGlnAlaSer	324
Db	2349	ACAGGTATCCACACCTTACTACAGTGCCTACCAACCTCACCGCA-----CTCTCAAGC	24020
Qy	325	SerGlyGlyTrpLeuThrTrpArgHisAsnGlyThrPheProAlaGlySerValSer	344
Db	2403	ACAGGCCCCACTGTATCTCACCGGGGATGTACACAGCCCAACCAAGCGGCACACGTCA	24632
Qy	345	ThyValLeuProGlnGlyPheAlaLeuGluArgTrpAspProAsnAspLyserrp---	363
Db	2463	GAGCGATCACCG-----GTGCACCAAGTGCATCTCCATGGGAC	2501
Qy	364	-----ThrAspPheAlaSerAlaGlyAspThrValThrPhe---	375
Db	2502	AACGGCAGAAAGTAAGCCCCCGACATGACCTCCACTCCACTCACGTGCTACCCCA	2561
Qy	376	ArgGlnValAlaValAspGluValValThrAsnAsnProAlaGlyGlyGlySerAla	395
Db	2562	ACCCCAATGTCACACAGCCCCACCCACGACGTGACTACCCCAACCCCAATGCCCACGC	2621
Qy	396	ProThrPheThrValArgValProProSerAsnAlaTrpThrAsnThrValPheArgAsn	415
Db	2622	CCGACCCCGACAGTGAAGTACCCCAACCCCAATGCCACAGC-----CCC	2666
Qy	416	ThrLeuLeuGlnThrArgProSerSerArgArgLeuGluLeuProMetProProAlaAsp	435
Db	2667	ACCTTGGGAAACAAAGTCTTACTCTCA---GCAGTGACTACCCCAACCCCAATGCC---	2720
Qy	436	PheGlyGlnThrValAlaAlaAsnAsnProLysIleGluGlnSerLeuLeuGlyGlnThrLeu	455


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Db 366425 GCTTCTTCAACAGCGCGCGGAGGATTCGGAATTCCTGAACCTCGGTCGCCGCTGT 366366
OY 589 eSerValleuysSerGluAlaThrSerSerIleIleuysValGluThrAlaV 609
Db 366365 CGGGCTACTCAATACCGCGCGGCTGGATCGGTCGCCCAACGGGCAACCATCT 366306
OY 609 aGlyAlaAlaInserGlyLeuAlaLysLeu-----ProGlyLeuLeuMetSerVal- 626
Db 366305 CGGGCTGTTGAACCGCACGCGCTGATCTCGCACGCCGGGTTCTTCCGGCATCG 366246
OY 627 -----ProG 628
Db 366245 GTAACTTGGCACCAACTGGCGGTTCTTGAAGGATTAACCGCAGCTATGTCACTG 366186
OY 628 lYLeuIleAlaAla-----ArgValArgAla 640
Db 366185 GGCACGACCGCTTCACTGCTCTCCAGAGGTGACAGCGCTTGGCCGATCGTAGACTC 366126
OY 640 rGArgArg 642
Db 366125 GCGCGAAG 366118

RESULT 15
US-09-103-840A-1/c
: Sequence 1, Application US/09103840A
: Patent No. 6294328
: GENERAL INFORMATION:
: APPLICANT: FLEISCHMAN, Robert D.
: APPLICANT: WHITE, Owen R.
: APPLICANT: FRASER, Claire M.
: APPLICANT: VENTER, John C.
: TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
: FILE REFERENCE: 24366-20007_00
: CURRENT APPLICATION NUMBER: US/09/103,840A
: CURRENT FILING DATE: 1998-06-24
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 1
: LENGTH: 441529
: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
: OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 5.02e+03 Length: 441529
Score: 121.00 Matches: 182
Percent Similarity: 31.25% Conservative: 63
Best Local Similarity: 23.21% Mismatches: 283
Query Match: 3.59% Indels: 260
DB: 4 Gaps: 40

US-09-677-653a-50 (1-647) x US-09-103-840A-1 (1-441529)
OY 31 GATGATGASnglnArGArGThrGlyArgGlnValSerProAspAsnPhetHr 50
Db 368152 GGGCAAGCTCAACACCGGCTGGCAACACCGGCGACA-TCAACACCGGCAACATCAACA 368094
OY 51 AlAlaAlaGlnAspLeuAlaGlnSerLeuAspAla-----AsnThrValThrPhe 67
Db 368093 CCGGCAAGCTCAACACCGGCAACATCAACCGGAGCTTCAACCTGGCGATCAACA 368034
OY 68 ProAlaAsnIleSerSerMetPro----- 75
Db 368033 CCGGCA-----GCTTCAACTCCGCTGACTACACACCGGCTACTTCAACCGGCTGACT 367980
OY 76 GluPheArgAsnTrpAlaLysGlyLysIleAspLeuAspSerAspSerIleGlyTrpTrp 95
Db 367979 ACAACACGCGGTGGCGCAACACCGGCAACGTCACACCGCGCGCTTCA----- 367932
OY 96 PheLysTrpLeuAspProAlaGlyAlaThrGluSerAlaArgAlaValGlyLysTrpSer 115

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Db 367931 -----TCATCCGCAATTACAGCAACGCGGTTCTTTCGGCA-GGTACTAC--- 367888
OY 116 LysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArgGluIleTrpAsn 135
Db 367887 -----CAAGGTTGATTCGCTTCCACACAGCATCAACCATCCGGAATTC----- 367843
OY 136 GluLysCysProValValThrAspAlaSerValProLeuAspGlyArgGlnTrpSerLeu 155
Db 367842 -----CCCTACCGCTACGACTTGAAGTGTTCACATGCAG-----ATA 367807
OY 156 SerIle-----PheSerPheProMetPheArg 164
Db 367806 CCCATCACCGGCGACCGCTGCTGCCACACCGCAACAGTTTCACCATTCGCCGTTTCCAG 367747
OY 165 -----ThrAlaTrpValAlaValAlaAsnValGluAsnLysGluMet-----Ser 179
Db 367746 ATACGAGTCTTGCTTGCTGCTCGCGGCTGCTTGTCACAGCATATATCGGCCCATCACG 367687
OY 180 LeuAspVal-----ValAsnAspLeuIleGlu-Tripe 190
Db 367686 ATCGATGTCATCAAGTCAATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 367627
OY 190 uAsnAsnLeuAlaAspTrpArgTrpValValAspSerGluGlnTrpIleAsnPhetHrAs 210
Db 367626 GGCACCGCGCGCTGCGCGCGGATCCCATCCGCAATCCGCAATCCGCAATCCGCGGTTTC 367567
OY 210 nAspThrThrTrpTrpValArgIleArgValLeuArgProThrTrpAspValProAspTr 230
Db 367566 GGCACCTGCAACACCGCGCGCGGCTGCGGTT-----TCTTCCACACCGCGGCC 367519
OY 230 oThrGluGlyLeuValArgThrValSerAspTrpArgLeu-----ThrTrpLysAlaI 248
Db 367518 G-----GCCATGATCGGGCTTCCGGGATTCGGGCGGCCCGGC 367483
OY 248 eHrcysGluAla-----AsnMetProThrLeuValAspGlnGlyPheTrpIleGlyLys 266
Db 367482 AACATGCGGCTCGCGGAACTTCGCGCTGCG-AATTCGCGCTTCTTAAACCGCGCGG 367424
OY 267 -----GlnTrpAlaLeuThrProThrSerLeuProGlnTrp-- 278
Db 367423 CTGGGCAATTGGGCTTCACTGAATTCGCGCGCTGCAAGTGGCTGCGCAACCTGGG 367364
OY 279 -----AspValSerGluAlaTrpAlaLeuHisThrLeuThrPheAlaArgProSerSerAl 297
Db 367363 CAACACATCTGCGGCTGCAACACGAGCAGCTGACCTCGGAGCGCGCGCTTGG 367304
OY 297 aAlaAlaLeuAlaPheValTrpAlaGlyLeu-ProGln-----GlyGlyThrAlaProAla- 315
Db 367303 CTCGGGCAATCGCAACATTCGCGGCAACCTGCGCGCTGTTCTTCGACACACCGGCA 367244
OY 315 ----- 315
Db 367243 CCGTACGCTGAATTCGCGGCTCGCAACACGCGCGCTCAACCGCGGCAATCGGCAACT 367184
OY 316 -----GlyThrProAlaTrpLeuGlnAlaSer 325
Db 367183 GGGCAGCGCAACATCGGCTTGTTAATACCGGCGCACTCAACCTCGGCAATCGGCAACT 367124
OY 325 eRgLyGlyTrpLeuThrTrpArgHisAsnGlyThrPheProAlaGlySerValSerT 345
Db 367123 CG-----GCGACCTCAACTTCGCGGCGGCGGCAACATCGG 367091
OY 345 TrpValLeuProGluGlyPheAlaLeuGluAlaGlyTrpAspProAsnAspLysSer----- 362
Db 367090 CGGTAAACAATCGGCA-----TCGCCAACAACCGGAGATCTTGATAT 367049
OY 363 -----TriPThrAspPheAlaSer----- 368
Db 367048 CGGCTTGGCAACTGCGGCACTTCACATCGGCTTGGCAATTCGCGGCGAGCAACACT 366989
OY 369 -----AlaGlyAspThrValThrPheArgGlnValAla----- 379

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Db 366988 GGGCTTTGGCAACGGCGAGCTACAAATCGGCTTCGGACTCGGACGACAACCT 366929
QY 380 -----ValaspGluValValThrAsnAsp 389
Db 366928 GGGCTTTGCCAACCGGAGCTACAAATCGGCTTCGGCAATACGGTAACAACAACAT 366869
QY 389 rolaAGlyGlySerAlaProThrPheThrValArgValProPheAsnAlaTyr 409
Db 366868 CGGCGTCGGGCTCAGCGGCAACGGCCAGATCGGATCGGACGCTCAACTCGGCGACCA 366809
QY 409 hrAsnThrValPheArgAsnThrLeuLeuGluThrArgProSerSerArgArgLeuGlu 428
Db 366808 CAACATCGGCGCTTCACTCCGAGCAACATCGGGTCTTCACTCGGCGACCGG 366749
QY 429 -----LeuProMetProProAlaAspPheGlyGlnThrValAlaAsnA 443
Db 366748 CAACGTGGGATCTTAACACCGGCAACCTTCGGCTCGCAACTCGGCGGCTT 366689
QY 443 snProLysIleGluInserLeuLeuLysGluThrLeuGlyCysTyrLeuValHisSerL 463
Db 366688 CAACACCGGATCGGCAACGGCGGAGCAACACGCGGCTTCAACCCGGGAGCT 366629
QY 463 ysketaArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaValSerPheA 483
Db 366628 CA-----ACACCGGAGCTTCAACCCGGGAGCTTCAAC-A 366594
QY 483 sn-----AsnProGlyTyrGluArgThrArgAspLeu-----ProAspTyr---T 497
Db 366593 CCGGCGGCTTCAACCGGCGAGTGGCAACACGCGGCTACCTCAACACCGGAGTACACAA 366534
QY 497 hrGlyIleArgAspSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArgSerL 517
Db 366533 CGGCGCTGGCGAACACGGGAGTGTGACACCGCTGCG-----TTCATTACCG 366486
QY 517 euSerHisSerCysSer---IleValThrLysThrTyrGlnGlyTyrGluGlyValThrA 536
Db 366485 GCAGCTACAGCAGCGGCTTCTTGTGGTGGCAGTATCAGGCGCTGATCGGCTGGCGG 366426
QY 536 snValAsnThrProPhe-----GlyGlnPheAlaHisAlaGlyLeuLeuLysAsnGluG 554
Db 366425 TGTGGGCAATTCGGTACCCCGGCTACTTC----- 366394
QY 554 IuIleLeuCysIleuAlaAspAspLeuAlaThrArgLeuThrGlyValTyrProAlaThrA 574
Db 366393 -----AACCTCACTGGC---GGCCGCTGCTCG 366369
QY 574 spAsnDhe-----AlaAlaAlaValSerAlaPhe-----AlaAlaAsnMetLeuS 589
Db 366368 GCTTCTTCAACGCGCGCGGAGGTATCGGATTCGTGAACCTCGGTGGCGGCTGT 366309
QY 589 erSerValLeuLysSerGluAlaThrSerSerIleIleLysSerValGlyGluThrAlaV 609
Db 366308 CGGCGTACCTCACTACCGGCGGCTGGATCGGCTGCGCAACGTGGCGCAACCATCT 366249
QY 609 alGlyAlaAlaGlnSerGlyLeuAlaLysLeu-----ProGlyLeuLeuMetSerVal- 626
Db 366248 CGGCGTGTGTGAACGCGGCGGCTGTGATCTCGGACGCGGCGGTCTTCCGGCATCG 366189
QY 627 -----ProG 628
Db 366188 GTAACCTTGGCAACCACTGGCGGTTCTTTAGGGATTAACGCGAGTATGTACACTG 366129
QY 628 LyrLysIleAlaAla-----ArgValArgAla-----ArgArgAlaA 640
Db 366128 GGGCAACGAGCGCTTCACTGCTTCCAGAGTGAAGCGCTTTGCCGATGTAGACTC 366069
QY 640 rgaArgArg 642
Db 366068 GGGGGAAG 366061
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